

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:06 ; Search time 43.3077 Seconds  
(without alignments)  
71.766 Million cell updates/sec

Title: US-09-787-443A-2

Perfect score: 11

Sequence: 1 AKKERQRKDTQ 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 22883

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : A\_Geneseq\_29Jan04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query				Description
			Match	Length	DB	ID	
1	11	100.0	11	3	AAY88528		Aay88528 NCAM Ig1
2	11	100.0	11	3	AAY88561		Aay88561 NCAM Ig1
3	11	100.0	11	5	ABG69330		Abg69330 Human neu
4	4	36.4	11	2	AAR37430		Aar37430 Promega p
5	4	36.4	11	2	AAR96841		Aar96841 Human moe
6	4	36.4	11	2	AAW09653		Aaw09653 Labelled
7	4	36.4	11	2	AAW11749		Aaw11749 T-cell re
8	4	36.4	11	2	AAW11750		Aaw11750 T-cell re
9	4	36.4	11	2	AAY31014		Aay31014 Non-cross

10	4	36.4	11	3	AAY88545	Aay88545 NCAM Ig1
11	4	36.4	11	4	ABP19679	Abp19679 HIV B62 s
12	4	36.4	11	4	ABP17507	Abp17507 HIV B27 s
13	4	36.4	11	4	ABP14260	Abp14260 HIV A02 s
14	4	36.4	11	4	ABP16618	Abp16618 HIV A24 s
15	4	36.4	11	4	ABP24378	Abp24378 HIV A24 m
16	4	36.4	11	4	ABP14259	Abp14259 HIV A02 s
17	4	36.4	11	4	ABP16617	Abp16617 HIV A24 s
18	4	36.4	11	4	ABP16616	Abp16616 HIV A24 s
19	4	36.4	11	5	ABG69345	Abg69345 Human neu
20	4	36.4	11	5	AAO18039	Aao18039 Human imm
21	3	27.3	11	1	AAP60142	Aap60142 Type 3 pe
22	3	27.3	11	1	AAP71164	Aap71164 Peptide w
23	3	27.3	11	1	AAP90643	Aap90643 Signal pe
24	3	27.3	11	2	AAR02183	Aar02183 Peptide w
25	3	27.3	11	2	AAR06031	Aar06031 Oligopept
26	3	27.3	11	2	AAR08092	Aar08092 Antifreez
27	3	27.3	11	2	AAR15673	Aar15673 Asn-resid
28	3	27.3	11	2	AAR12168	Aar12168 Neuropept
29	3	27.3	11	2	AAR12171	Aar12171 Neuropept
30	3	27.3	11	2	AAR12173	Aar12173 Neuropept
31	3	27.3	11	2	AAR22743	Aar22743 Non-A, No
32	3	27.3	11	2	AAR35381	Aar35381 Amphiphil
33	3	27.3	11	2	AAR32351	Aar32351 Human Fac
34	3	27.3	11	2	AAR33973	Aar33973 Amphiphil
35	3	27.3	11	2	AAR31163	Aar31163 C-termina
36	3	27.3	11	2	AAR34248	Aar34248 Mutant HT
37	3	27.3	11	2	AAR30442	Aar30442 Synthetic
38	3	27.3	11	2	AAR30463	Aar30463 Synthetic
39	3	27.3	11	2	AAR30478	Aar30478 Synthetic
40	3	27.3	11	2	AAR41495	Aar41495 TNF inhib
41	3	27.3	11	2	AAR39369	Aar39369 Human gly
42	3	27.3	11	2	AAR45132	Aar45132 Amphiphil
43	3	27.3	11	2	AAR34421	Aar34421 Hepatitis
44	3	27.3	11	2	AAR55163	Aar55163 Fragment
45	3	27.3	11	2	AAR50563	Aar50563 Amphiphil
46	3	27.3	11	2	AAR55987	Aar55987 Ion chann
47	3	27.3	11	2	AAR59065	Aar59065 Cancer tr
48	3	27.3	11	2	AAR56948	Aar56948 Peptide w
49	3	27.3	11	2	AAR50448	Aar50448 Amphiphil
50	3	27.3	11	2	AAR51276	Aar51276 Meningoco
51	3	27.3	11	2	AAR51277	Aar51277 Meningoco
52	3	27.3	11	2	AAR82678	Aar82678 V8 fragme
53	3	27.3	11	2	AAW21496	Aaw21496 Hepatitis
54	3	27.3	11	2	AAW21220	Aaw21220 Farnesyl
55	3	27.3	11	2	AAR76917	Aar76917 Thymosin
56	3	27.3	11	2	AAR84537	Aar84537 Hepatitis
57	3	27.3	11	2	AAR90259	Aar90259 Ion-chann
58	3	27.3	11	2	AAR91788	Aar91788 Ion-chann
59	3	27.3	11	2	AAR91787	Aar91787 Ion-chann
60	3	27.3	11	2	AAR87902	Aar87902 Neuropept
61	3	27.3	11	2	AAW49555	Aaw49555 Human leu
62	3	27.3	11	2	AAR96835	Aar96835 Human neu
63	3	27.3	11	2	AAR85318	Aar85318 Human ret
64	3	27.3	11	2	AAW18499	Aaw18499 Amino-ter
65	3	27.3	11	2	AAW24438	Aaw24438 Nucleic a
66	3	27.3	11	2	AAW34642	Aaw34642 Control p

67	3	27.3	11	2	AAW09909	Aaw09909 Prostate
68	3	27.3	11	2	AAW10140	Aaw10140 Hepatitis
69	3	27.3	11	2	AAW62116	Aaw62116 Human MDM
70	3	27.3	11	2	AAW66523	Aaw66523 Amphiphil
71	3	27.3	11	2	AAW80589	Aaw80589 src-famil
72	3	27.3	11	2	AAW64653	Aaw64653 Synthetic
73	3	27.3	11	2	AAW51825	Aaw51825 Peptide Y
74	3	27.3	11	2	AAW84029	Aaw84029 Human CYP
75	3	27.3	11	2	AAW84023	Aaw84023 Human CYP
76	3	27.3	11	2	AAW84026	Aaw84026 Human CYP
77	3	27.3	11	2	AAW50263	Aaw50263 HIV-1 tat
78	3	27.3	11	2	AAY30700	Aay30700 Apo-B100
79	3	27.3	11	2	AAY30698	Aay30698 Apo-B100
80	3	27.3	11	2	AAW72988	Aaw72988 Bovine be
81	3	27.3	11	2	AAY05150	Aay05150 HIV Tat p
82	3	27.3	11	2	AAY39666	Aay39666 Tat-inhib
83	3	27.3	11	2	AAY39664	Aay39664 Tat-inhib
84	3	27.3	11	2	AAY39667	Aay39667 Tat-inhib
85	3	27.3	11	2	AAY39662	Aay39662 Tat-inhib
86	3	27.3	11	2	AAY39663	Aay39663 Tat-inhib
87	3	27.3	11	2	AAY39665	Aay39665 Tat-inhib
88	3	27.3	11	2	AAY39669	Aay39669 Tat-inhib
89	3	27.3	11	2	AAW97477	Aaw97477 Antigenic
90	3	27.3	11	2	AAY05415	Aay05415 Tat pepti
91	3	27.3	11	2	AAW81004	Aaw81004 S. cerevi
92	3	27.3	11	2	AAY05440	Aay05440 Bronchodi
93	3	27.3	11	2	AAY25084	Aay25084 TAT domai
94	3	27.3	11	2	AAY25075	Aay25075 TAT trans
95	3	27.3	11	2	AAY10761	Aay10761 Peptide u
96	3	27.3	11	2	AAY10750	Aay10750 Peptide u
97	3	27.3	11	2	AAY10762	Aay10762 Peptide u
98	3	27.3	11	3	AAY66823	Aay66823 T cell an
99	3	27.3	11	3	AAB27088	Aab27088 Beta-cate
100	3	27.3	11	3	AAB16472	Aab16472 Linear pe

#### ALIGNMENTS

RESULT 1  
 AAY88528  
 ID AAY88528 standard; peptide; 11 AA.  
 XX  
 AC AAY88528;  
 XX  
 DT 07-AUG-2000 (first entry)  
 XX  
 DE NCAM Ig1 binding peptide D3.  
 XX  
 KW NCAM; neural cell adhesion molecule; Ig1; immunoglobulin domain 1;  
 KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;  
 KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;  
 KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;  
 KW treatment; prosthetic nerve guide; treatment; nervous system.  
 XX  
 OS Synthetic.  
 XX

PN WO200018801-A2.  
XX  
PD 06-APR-2000.  
XX  
PF 23-SEP-1999; 99WO-DK000500.  
XX  
PR 29-SEP-1998; 98DK-00001232.  
PR 29-APR-1999; 99DK-00000592.  
XX  
PA (RONN/) RONN L C B.  
PA (BOCK/) BOCK E.  
PA (HOLM/) HOLM A.  
PA (OLSE/) OLSEN M.  
PA (OSTE/) OSTERGAARD S.  
PA (JENS/) JENSEN P H.  
PA (POUL/) POULSEN F M.  
PA (SORO/) SOROKA V.  
PA (RALE/) RALETS I.  
PA (BERE/) BEREZIN V.  
XX  
PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;  
PI Poulsen FM, Soroka V, Ralets I, Berezin V;  
XX  
DR WPI; 2000-293111/25.  
XX  
PT Compositions that bind neural cell adhesion molecules useful for treating  
PT disorders of the nervous system and muscles e.g. Alzheimer's and  
PT Parkinson's diseases.  
XX  
PS Claim 20; Page 82; 119pp; English.  
XX  
CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.  
CC NCAM is found in three forms, two of which are transmembrane forms, while  
CC the third is attached via a lipid anchor to the cell membrane. All three  
CC NCAM forms have an extracellular structure consisting five immunoglobulin  
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-  
CC terminal. The present sequence represents a peptide which binds to the  
CC NCAM Ig1 domain. The peptide can be used in a compound which binds to  
CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite  
CC outgrowth from NCAM presenting cells, and is also capable of promoting  
CC the proliferation of NCAM presenting cells. The compound may be used in  
CC the treatment of normal, degenerated or damaged NCAM presenting cells.  
CC The compound may in particular be used to treat diseases of the central  
CC and peripheral nervous systems such as post operative nerve damage,  
CC traumatic nerve damage, impaired myelination of nerve fibres, conditions  
CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,  
CC dementias, sclerosis, nerve degeneration associated with diabetes  
CC mellitus, disorders affecting the circadian clock or neuro-muscular  
CC transmission and schizophrenia. Conditions affecting the muscles may also  
CC be treated with the compound, such as conditions associated with impaired  
CC function of neuromuscular connections (e.g. genetic or traumatic shock or  
CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas  
CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,  
CC liver and bowel may also be treated using the compound. The compound is  
CC used in a prosthetic nerve guide, and also to stimulate the ability to  
CC learn, and to stimulate the memory of a subject  
XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKERQRKDTQ 11  
|||||||||||  
Db 1 AKKERQRKDTQ 11

RESULT 2

AAY88561

ID AAY88561 standard; peptide; 11 AA.

XX

AC AAY88561;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Ig1 binding peptide D3 used as a control peptide.

XX

KW NCAM; neural cell adhesion molecule; Ig1; immunoglobulin domain 1;  
KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;  
KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;  
KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;  
KW treatment; prosthetic nerve guide; treatment; nervous system.

XX

OS Synthetic.

XX

PN WO200018801-A2.

XX

PD 06-APR-2000.

XX

PF 23-SEP-1999; 99WO-DK000500.

XX

PR 29-SEP-1998; 98DK-00001232.

PR 29-APR-1999; 99DK-00000592.

XX

PA (RONN/) RONN L C B.

PA (BOCK/) BOCK E.

PA (HOLM/) HOLM A.

PA (OLSE/) OLSEN M.

PA (OSTE/) OSTERGAARD S.

PA (JENS/) JENSEN P H.

PA (POUL/) POULSEN F M.

PA (SORO/) SOROKA V.

PA (RALE/) RALETS I.

PA (BERE/) BEREZIN V.

XX

PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;

PI Poulsen FM, Soroka V, Ralets I, Berezin V;

XX

DR WPI; 2000-293111/25.

XX

PT Compositions that bind neural cell adhesion molecules useful for treating  
PT disorders of the nervous system and muscles e.g. Alzheimer's and  
PT Parkinson's diseases.

XX

PS Example 5; Fig 7; 119pp; English.

XX

CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.  
CC NCAM is found in three forms, two of which are transmembrane forms, while  
CC the third is attached via a lipid anchor to the cell membrane. All three  
CC NCAM forms have an extracellular structure consisting five immunoglobulin  
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-  
CC terminal. The invention relates to a compound containing a peptide which  
CC binds to the NCAM Ig1 domain. The compound binds to NCAM-Ig1/Ig2 domains,  
CC and is capable of stimulating or promoting neurite outgrowth from NCAM  
CC presenting cells, and is also capable of promoting the proliferation of  
CC NCAM presenting cells. The present sequence represents a control peptide  
CC used in the identification of those binding peptides which can be used in  
CC the compound. The compound may be used in the treatment of normal,  
CC degenerated or damaged NCAM presenting cells. The compound may in  
CC particular be used to treat diseases of the central and peripheral  
CC nervous systems such as post operative nerve damage, traumatic nerve  
CC damage, impaired myelination of nerve fibres, conditions resulting from a  
CC stroke, Parkinson's disease, Alzheimer's disease, dementias, sclerosis,  
CC nerve degeneration associated with diabetes mellitus, disorders affecting  
CC the circadian clock or neuro-muscular transmission and schizophrenia.  
CC Conditions affecting the muscles may also be treated with the compound,  
CC such as conditions associated with impaired function of neuromuscular  
CC connections (e.g. genetic or traumatic shock or traumatic atrophic muscle  
CC disorders). Conditions of the gonads, pancreas (e.g. diabetes mellitus  
CC types I and II), kidney (e.g. nephrosis), heart, liver and bowel may also  
CC be treated using the compound. The compound is used in a prosthetic nerve  
CC guide, and also to stimulate the ability to learn, and to stimulate the  
CC memory of a subject

XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 AKKERQRKDTQ 11  
|||||||||||

Db

1 AKKERQRKDTQ 11

RESULT 3

ABG69330

ID ABG69330 standard; peptide; 11 AA.

XX

AC ABG69330;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human neural cell adhesion molecule (NCAM) peptide #2.

XX

KW Human; neural cell adhesion molecule; NCAM; heart muscle cell survival;  
KW acute myocardial infarction; central nervous system disorder; stroke;  
KW peripheral nervous system disorder; postoperative nerve damage;  
KW traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia;  
KW postischaemic damage; multiinfarct dementia; multiple sclerosis;

KW nerve degeneration; diabetes mellitus; neuro-muscular degeneration;  
KW Alzheimer's disease; Parkinson's disease;  
KW Huntington's disease. atrophic muscle disorder; gonad degeneration;  
KW nephrosis.  
XX  
OS Homo sapiens.  
XX  
PN WO200247719-A2.  
XX  
PD 20-JUN-2002.  
XX  
PF 12-DEC-2001; 2001WO-DK000822.  
XX  
PR 12-DEC-2000; 2000DK-00001863.  
XX  
PA (ENKA-) ENKAM PHARM AS.  
XX  
PI Bock E, Berezin V, Kohler LB;  
XX  
DR WPI; 2002-583473/62.  
XX  
PT Use of a compound comprising a peptide of neural cell adhesion molecule,  
PT in the preparation of medicament for preventing death of cells presenting  
PT NCAM or NCAM ligand and treating central nervous system diseases.  
XX  
PS Claim 26; Page 39; 57pp; English.  
XX  
CC The invention relates to use of a compound (I) comprising a peptide which  
CC comprises at least 5 contiguous amino acid residues of a sequence of the  
CC neural cell adhesion molecule (NCAM), its fragment, variant or its mimic,  
CC for the preparation of a medicament for preventing death of cells  
CC presenting the NCAM or an NCAM ligand. (I) is useful in the preparation  
CC of a medicament for preventing death of cells presenting the NCAM or an  
CC NCAM ligand. The medicament is for the stimulation of the survival of  
CC heart muscle cells, such as survival after acute myocardial infarction.  
CC The medicament is for the treatment of diseases or conditions of the  
CC central and peripheral nervous system, such as postoperative nerve  
CC damage, traumatic nerve damage, e.g. resulting from spinal cord injury,  
CC impaired myelination of nerve fibres, postischaemic damage, e.g.  
CC resulting from a stroke, multiinfarct dementia, multiple sclerosis, nerve  
CC degeneration associated with diabetes mellitus, neuro-muscular  
CC degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease and  
CC Huntington's disease. The medicament is for the treatment of diseases or  
CC conditions of the muscles including conditions with impaired function of  
CC neuro-muscular connections, such as genetic or traumatic atrophic muscle  
CC disorders, and for the treatment of diseases of conditions of various  
CC organs, such as degenerative conditions of the gonads, pancreas (e.g.  
CC diabetes mellitus type I and II) and kidney (e.g. nephrosis). ABG69329-  
CC ABG69352 represent human NCAM peptides of the invention  
XX  
SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKERQRKDTQ 11

|||||||  
Db 1 AKKERQRKDTQ 11

RESULT 4  
AAR37430  
ID AAR37430 standard; peptide; 11 AA.  
XX  
AC AAR37430;  
XX  
DT 25-MAR-2003 (revised)  
DT 08-SEP-1993 (first entry)  
XX  
DE Promega peptide 5.  
XX  
KW Modified peptide substrate; non-radioactive; detection; dansyl;  
KW sulphorhodamine 101; lissamine; rhodamine; enzymes; phosphatases;  
KW protein kinases; proteases.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT /note= "detection tag= lissamine, Rhodamine"  
XX  
PN WO9310461-A1.  
XX  
PD 27-MAY-1993.  
XX  
PF 12-NOV-1992; 92WO-US009595.  
XX  
PR 12-NOV-1991; 91US-00791928.  
XX  
PA (PROM-) PROMEGA CORP.  
XX  
PI Shultz JW, White DH;  
XX  
DR WPI; 1993-182698/22.  
XX  
PT Quantitating presence or activity of enzyme - by incubating with modified  
PT peptide substrate and measuring the modified peptide prod.  
XX  
PS Claim 24; Page 27; 103pp; English.  
XX  
CC Promega peptide 5 is tagged with dansyl at residue 1 and may be used in a  
CC novel non-radioactive method of quantitating the presence or activity of  
CC an enzyme. The method can be used for rapid, specific and highly  
CC sensitive detection of enzymes such as protein kinases, phosphatases and  
CC proteases, esp. in this case protein kinase C. They can be used to study  
CC enzyme function in metabolism and in diagnosis of disease. They also  
CC allow quantitative determ. of the enzyme's activity. See also AAR37426-  
CC 36. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RQRK 8  
||||  
Db 3 RQRK 6

RESULT 5

AAR96841

ID AAR96841 standard; peptide; 11 AA.

XX

AC AAR96841;

XX

DT 29-NOV-1996 (first entry)

XX

DE Human moesin fragment, homologous to Neisseria Iga-alpha2.

XX

KW IgA protease precursor; IPP; bacterial polyprotein; autoimmune;  
KW viral infection; rheumatoid arthritis; AIDS; meningococcal bacteria;  
KW human small nuclear ribonucleoprotein-associated protein; Rsmb;  
KW Neisseria gonorrhoeae; R16.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 1

FT /note= "identical to corresponding residue in Neisseria  
gonorrhoeae Iga-alpha2"

FT Region 6..11

FT /note= "identical to sequence in Neisseria gonorrhoeae  
Iga-alpha2"

XX

PN WO9609395-A2.

XX

PD 28-MAR-1996.

XX

PF 21-SEP-1995; 95WO-EP003726.

XX

PR 21-SEP-1994; 94DE-04433708.

XX

PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX

PI Meyer TF, Pohlner J, Beck SC, Jose J, Woelk U, Lorenzen DR;

PI Oetzelberger KB;

XX

DR WPI; 1996-188456/19.

XX

PT Medicaments for treating auto-immune or viral diseases - contg.

PT substances interfering with bacterial poly:protein function.

XX

PS Claim 32; Fig 2; 117pp; German.

XX

CC The present sequence from human moesin has homology to a cleavage product  
CC from the Iga-alpha2 domain of the precursor of IgA-protease polyprotein  
CC (IPP) of Neisseria gonorrhoeae strain R16. The Neisseria IPP has been  
CC implicated in rheumatoid arthritis and other auto-immune diseases. The  
CC polyprotein also activates proviruses, including HIV. Substances which

CC interfere with the function of IPP from Neisseria will be useful for  
CC treating associated autoimmune diseases and viral infections. Peptides  
CC comprising the homology region sequences, whether from Neisseria or from  
CC humans, are claimed

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KERQ 6  
||||  
Db 2 KERQ 5

RESULT 6

AAW09653

ID AAW09653 standard; peptide; 11 AA.

XX

AC AAW09653;

XX

DT 25-MAR-2003 (revised)

DT 20-MAY-1997 (first entry)

XX

DE Labelled peptide substrate used in enzyme activity assay.

XX

KW Enzyme activity; assay; measurement; label; rhodamine; dansyl;  
KW non-radioactive; electrophoretic separation; protein kinase; protease;  
KW phosphatase.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "labelled with rhodamine B detection tag"

XX

PN US5580747-A.

XX

PD 03-DEC-1996.

XX

PF 21-JAN-1994; 94US-00185448.

XX

PR 12-NOV-1991; 91US-00791928.

XX

PA (PROM-) PROMEGA CORP.

XX

PI White DH, Shultz JW;

XX

DR WPI; 1997-033568/03.

XX

PT Non:radioactive assay for measuring enzyme activity - involving  
PT electrophoretic sepn. of labelled cleavage prod. from labelled peptide  
PT substrate.

XX

PS Claim 5; Col 39-40; 35pp; English.

XX

CC AAW09653 is a peptide substrate used in a non-radioactive assay for  
CC measuring enzyme activity. The assay comprises incubating the enzyme with  
CC the labelled peptide substrate to form a labelled peptide product;  
CC separating the product from the substrate by agarose gel electrophoresis  
CC and measuring the amount of product by detecting the label by  
CC fluorescence or chemiluminescence. The assay can be performed rapidly and  
CC with great sensitivity. This peptide is especially for determining  
CC protein kinase C activity, e.g. to study its function in metabolism or to  
CC screen for potential inhibitors. (Updated on 25-MAR-2003 to correct PF  
CC field.)

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQRK 8  
||||  
Db 3 RQRK 6

RESULT 7

AAW11749

ID AAW11749 standard; peptide; 11 AA.

XX

AC AAW11749;

XX

DT 04-NOV-1997 (first entry)

XX

DE T-cell receptor peptide V(beta)5.2 (49-59)F.

XX

KW T-cell receptor; TCR; V(beta)5.2; multiple sclerosis;  
KW rheumatoid arthritis; myasthenia gravis; encephalomyelitis; diabetes;  
KW inflammatory bowel disease; systemic lupus erythematosus; thyroiditis;  
KW therapy; diagnosis; vaccine.

XX

OS Synthetic.

XX

PN WO9640778-A1.

XX

PD 19-DEC-1996.

XX

PF 06-JUN-1996; 96WO-US009423.

XX

PR 07-JUN-1995; 95US-00476405.

XX

PA (CONN-) CONNECTIVE THERAPEUTICS INC.

XX

PI Vandenbark AA;

XX

DR WPI; 1997-099923/09.

XX

PT T cell receptor peptide derived from V(beta)-5 family - useful for  
PT treating e.g. multiple sclerosis, myasthenia gravis, diabetes, etc.

XX

PS Claim 9; Page 42; 54pp; English.

XX  
CC This sequence is a synthetic peptide based on amino acid residues 49-59  
CC of the V(beta)5.2 region (see AAW11767) of human T cell receptor (TCR).  
CC It is a specifically preferred peptide for use in a claimed method for  
CC the treatment, prevention or suppression of a T-cell mediated disease  
CC such as multiple sclerosis, rheumatoid arthritis, myasthenia gravis,  
CC encephalomyelitis, thyroiditis, diabetes, inflammatory bowel disease or  
CC systemic lupus erythematosus. Claimed TCR peptides (AAW11741-65) are  
CC derived from the V(beta)5 family, or are functional derivatives of  
CC V(beta)5 peptides  
XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERQR 7  
||||  
Db 7 ERQR 10

RESULT 8

AAW11750

ID AAW11750 standard; peptide; 11 AA.

XX  
AC AAW11750;

XX  
DT 04-NOV-1997 (first entry)

XX  
DE T-cell receptor peptide V(beta)5.2 (49-59) FV.

XX  
KW T-cell receptor; TCR; V(beta)5.2; multiple sclerosis;  
KW rheumatoid arthritis; myasthenia gravis; encephalomyelitis; diabetes;  
KW inflammatory bowel disease; systemic lupus erythematosus; thyroiditis;  
KW therapy; diagnosis; vaccine.

XX  
OS Synthetic.

XX  
FH Key Location/Qualifiers  
FT Misc-difference 2  
FT /note= "residue 2 is Tyr in V(beta)5.2 (49-59) F"

XX  
PN WO9640778-A1.

XX  
PD 19-DEC-1996.

XX  
PF 06-JUN-1996; 96WO-US009423.

XX  
PR 07-JUN-1995; 95US-00476405.

XX  
PA (CONN-) CONNECTIVE THERAPEUTICS INC.

XX  
PI Vandenbark AA;

XX  
DR WPI; 1997-099923/09.

XX

PT T cell receptor peptide derived from V(beta)-5 family - useful for  
PT treating e.g. multiple sclerosis, myasthenia gravis, diabetes, etc.  
XX  
PS Claim 9; Page 42; 54pp; English.  
XX  
CC This sequence is a synthetic peptide based on amino acid residues 49-59  
CC of the V(beta)5.2 region (see AAW11767) of human T cell receptor (TCR).  
CC It is a specifically preferred peptide for use in a claimed method for  
CC the treatment, prevention or suppression of a T-cell mediated disease  
CC such as multiple sclerosis, rheumatoid arthritis, myasthenia gravis,  
CC encephalomyelitis, thyroiditis, diabetes, inflammatory bowel disease or  
CC systemic lupus erythematosus. Claimed TCR peptides (AAW11741-65) are  
CC derived from the V(beta)5 family, or are functional derivatives of  
CC V(beta)5 peptides  
XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ERQR 7  
||||  
Db 7 ERQR 10

RESULT 9  
AAY31014  
ID AAY31014 standard; peptide; 11 AA.  
XX  
AC AAY31014;  
XX  
DT 21-OCT-1999 (first entry)  
XX  
DE Non-crosslinked protein particle peptide 63.  
XX  
KW Non-crosslinked protein particle; diagnostic; therapy; monodisperse;  
KW albumin; haemoglobin; nanometer; micrometer; clearance.  
XX  
OS Synthetic.  
XX  
PN US5945033-A.  
XX  
PD 31-AUG-1999.  
XX  
PF 12-NOV-1996; 96US-00747137.  
XX  
PR 15-JAN-1991; 91US-00641720.  
PR 13-OCT-1992; 92US-00959560.  
PR 01-JUN-1993; 93US-00069831.  
PR 14-MAR-1994; 94US-00212546.  
XX  
PA (HEMO-) HEMOSPHERE INC.  
XX  
PI Yen RCK;  
XX  
DR WPI; 1999-508153/42.

XX  
PT Non-crosslinked protein particles for therapeutic and diagnostic use.  
XX  
PS Example 22; Col 77-78; 65pp; English.  
XX  
CC This invention describes a novel aqueous suspension of monodisperse  
CC particles on non-crosslinked, non-denatured albumin (50-5000 nm) which is  
CC stable against dissolving upon dilution with an alcohol-free aqueous  
CC medium. The method involves (a) forming an aqueous solution containing  
CC albumin and hemoglobin and (b) treating the aqueous solution with an  
CC alcohol to cause the solution to become turbid. The particles are useful  
CC as agents for in vivo administration, either of their own administration  
CC or as a vehicle for other therapeutic or diagnostic agents. The method  
CC permits the formation of albumin and hemoglobin particles in the  
CC nanometer and micrometer size range, in a form closer to their natural  
CC form than the forms of the prior art. The particles therefore constitute  
CC a more closely controlled agent for in vivo administration, with greater  
CC ease of clearance from the body after their period of usefulness.  
CC AAY30952-Y31135 represent peptides used in the method of the invention  
XX  
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQRK 8  
||||  
Db 3 RQRK 6

RESULT 10  
AAY88545  
ID AAY88545 standard; peptide; 11 AA.  
XX  
AC AAY88545;  
XX  
DT 07-AUG-2000 (first entry)  
XX  
DE NCAM Ig1 binding peptide #17.  
XX  
KW NCAM; neural cell adhesion molecule; Ig1; immunoglobulin domain 1;  
KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;  
KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;  
KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;  
KW treatment; prosthetic nerve guide; treatment; nervous system.  
XX  
OS Synthetic.  
XX  
PN WO200018801-A2.  
XX  
PD 06-APR-2000.  
XX  
PF 23-SEP-1999; 99WO-DK000500.  
XX  
PR 29-SEP-1998; 98DK-00001232.  
PR 29-APR-1999; 99DK-00000592.

XX  
PA (RONN/) RONN L C B.  
PA (BOCK/) BOCK E.  
PA (HOLM/) HOLM A.  
PA (OLSE/) OLSEN M.  
PA (OSTE/) OSTERGAARD S.  
PA (JENS/) JENSEN P H.  
PA (POUL/) POULSEN F M.  
PA (SORO/) SOROKA V.  
PA (RALE/) RALETS I.  
PA (BERE/) BEREZIN V.  
XX  
PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;  
PI Poulsen FM, Soroka V, Ralets I, Berezin V;  
XX  
DR WPI; 2000-293111/25.  
XX  
PT Compositions that bind neural cell adhesion molecules useful for treating  
PT disorders of the nervous system and muscles e.g. Alzheimer's and  
PT Parkinson's diseases.  
XX  
PS Example 4; Page 25; 119pp; English.  
XX  
CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.  
CC NCAM is found in three forms, two of which are transmembrane forms, while  
CC the third is attached via a lipid anchor to the cell membrane. All three  
CC NCAM forms have an extracellular structure consisting five immunoglobulin  
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-  
CC terminal. The present sequence represents a peptide which binds to the  
CC NCAM Ig1 domain. The peptide can be used in a compound which binds to  
CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite  
CC outgrowth from NCAM presenting cells, and is also capable of promoting  
CC the proliferation of NCAM presenting cells. The compound may be used in  
CC the treatment of normal, degenerated or damaged NCAM presenting cells.  
CC The compound may in particular be used to treat diseases of the central  
CC and peripheral nervous systems such as post operative nerve damage,  
CC traumatic nerve damage, impaired myelination of nerve fibres, conditions  
CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,  
CC dementias, sclerosis, nerve degeneration associated with diabetes  
CC mellitus, disorders affecting the circadian clock or neuro-muscular  
CC transmission and schizophrenia. Conditions affecting the muscles may also  
CC be treated with the compound, such as conditions associated with impaired  
CC function of neuromuscular connections (e.g. genetic or traumatic shock or  
CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas  
CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,  
CC liver and bowel may also be treated using the compound. The compound is  
CC used in a prosthetic nerve guide, and also to stimulate the ability to  
CC learn, and to stimulate the memory of a subject  
XX  
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKE 4  
||||

RESULT 11  
ABP19679  
ID ABP19679 standard; peptide; 11 AA.  
XX  
AC ABP19679;  
XX  
DT 11-SEP-2003 (revised)  
DT 15-JUL-2002 (first entry)  
XX  
DE HIV B62 super motif vpu peptide #17.  
XX  
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO200124810-A1.  
XX  
PD 12-APR-2001.  
XX  
PF 05-OCT-2000; 2000WO-US027766.  
XX  
PR 05-OCT-1999; 99US-00412863.  
XX  
PA (EPIM-) EPIMMUNE INC.  
XX  
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
PI Baker DM, Celis E, Kubo RT, Grey HM;  
XX  
DR WPI; 2001-354887/37.  
XX  
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.  
XX  
PS Claim 32; Page 272; 448pp; English.  
XX  
CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced

CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQRK 8  
|||  
Db 3 RQRK 6

RESULT 12

ABP17507

ID ABP17507 standard; peptide; 11 AA.

XX

AC ABP17507;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV B27 super motif rev peptide #18.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.

XX

PS Claim 32; Page 227; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ERQR 7  
|||  
Db 6 ERQR 9

RESULT 13

ABP14260

ID ABP14260 standard; peptide; 11 AA.

XX

AC ABP14260;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV A02 super motif vpu peptide #43.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX  
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
PI Baker DM, Celis E, Kubo RT, Grey HM;  
XX  
DR WPI; 2001-354887/37.  
XX  
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.  
XX  
PS Claim 32; Page 160; 448pp; English.  
XX  
CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQRK 8  
||||  
Db 3 RQRK 6

RESULT 14  
ABP16618  
ID ABP16618 standard; peptide; 11 AA.  
XX  
AC ABP16618;  
XX  
DT 11-SEP-2003 (revised)  
DT 15-JUL-2002 (first entry)  
XX  
DE HIV A24 super motif vpu peptide #33.  
XX  
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO200124810-A1.  
XX  
PD 12-APR-2001.  
XX  
PF 05-OCT-2000; 2000WO-US027766.  
XX  
PR 05-OCT-1999; 99US-00412863.  
XX  
PA (EPIM-) EPIMMUNE INC.  
XX  
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
PI Baker DM, Celis E, Kubo RT, Grey HM;  
XX  
DR WPI; 2001-354887/37.  
XX  
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.  
XX  
PS Claim 32; Page 208; 448pp; English.  
XX  
CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABL25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABL11501 to ABL25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQRK 8  
Db 3 RQRK 6

RESULT 15  
ABP24378  
ID ABP24378 standard; peptide; 11 AA.  
XX  
AC ABP24378;  
XX  
DT 11-SEP-2003 (revised)  
DT 15-JUL-2002 (first entry)  
XX  
DE HIV A24 motif vpu peptide #9.  
XX  
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO200124810-A1.  
XX  
PD 12-APR-2001.  
XX  
PF 05-OCT-2000; 2000WO-US027766.  
XX  
PR 05-OCT-1999; 99US-00412863.  
XX  
PA (EPIM-) EPIMMUNE INC.  
XX  
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
PI Baker DM, Celis E, Kubo RT, Grey HM;  
XX  
DR WPI; 2001-354887/37.  
XX  
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.  
XX  
PS Claim 32; Page 368; 448pp; English.  
XX  
CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as

CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQRK 8  
||||

Db 7 RQRK 10

RESULT 16

ABP14259

ID ABP14259 standard; peptide; 11 AA.

XX

AC ABP14259;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV A02 super motif vpu peptide #42.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.

XX

PS Claim 32; Page 160; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may

CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQRK 8  
|||  
Db 4 RQRK 7

RESULT 17  
ABP16617  
ID ABP16617 standard; peptide; 11 AA.  
XX  
AC ABP16617;  
XX  
DT 11-SEP-2003 (revised)  
DT 15-JUL-2002 (first entry)  
XX  
DE HIV A24 super motif vpu peptide #32.  
XX  
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO200124810-A1.  
XX  
PD 12-APR-2001.  
XX  
PF 05-OCT-2000; 2000WO-US027766.  
XX  
PR 05-OCT-1999; 99US-00412863.  
XX  
PA (EPIM-) EPIMMUNE INC.  
XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
PI Baker DM, Celis E, Kubo RT, Grey HM;  
XX  
DR WPI; 2001-354887/37.  
XX  
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.  
XX  
PS Claim 32; Page 208; 448pp; English.  
XX  
CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQRK 8  
      ||||  
Db 4 RQRK 7

RESULT 18  
ABP16616  
ID ABP16616 standard; peptide; 11 AA.  
XX  
AC ABP16616;  
XX  
DT 11-SEP-2003 (revised)  
DT 15-JUL-2002 (first entry)  
XX  
DE HIV A24 super motif vpu peptide #31.  
XX  
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO200124810-A1.  
XX  
PD 12-APR-2001.  
XX  
PF 05-OCT-2000; 2000WO-US027766.  
XX  
PR 05-OCT-1999; 99US-00412863.  
XX  
PA (EPIM-) EPIMMUNE INC.  
XX  
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
PI Baker DM, Celis E, Kubo RT, Grey HM;  
XX  
DR WPI; 2001-354887/37.  
XX  
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.  
XX  
PS Claim 32; Page 208; 448pp; English.  
XX  
CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABL25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABL11501 to ABL25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQRK 8  
Db 7 RQRK 10

RESULT 19  
ABG69345  
ID ABG69345 standard; peptide; 11 AA.  
XX  
AC ABG69345;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human neural cell adhesion molecule (NCAM) peptide #17.  
XX  
KW Human; neural cell adhesion molecule; NCAM; heart muscle cell survival;  
KW acute myocardial infarction; central nervous system disorder; stroke;  
KW peripheral nervous system disorder; postoperative nerve damage;  
KW traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia;  
KW postischaemic damage; multiinfarct dementia; multiple sclerosis;  
KW nerve degeneration; diabetes mellitus; neuro-muscular degeneration;  
KW Alzheimer's disease; Parkinson's disease;  
KW Huntington's disease. atrophic muscle disorder; gonad degeneration;  
KW nephrosis.  
XX  
OS Homo sapiens.  
XX  
PN WO200247719-A2.  
XX  
PD 20-JUN-2002.  
XX  
PF 12-DEC-2001; 2001WO-DK000822.  
XX  
PR 12-DEC-2000; 2000DK-00001863.  
XX  
PA (ENKA-) ENKAM PHARM AS.  
XX  
PI Bock E, Berezin V, Kohler LB;  
XX  
DR WPI; 2002-583473/62.  
XX  
PT Use of a compound comprising a peptide of neural cell adhesion molecule,  
PT in the preparation of medicament for preventing death of cells presenting  
PT NCAM or NCAM ligand and treating central nervous system diseases.  
XX  
PS Disclosure; Page 16; 57pp; English.  
XX  
CC The invention relates to use of a compound (I) comprising a peptide which  
CC comprises at least 5 contiguous amino acid residues of a sequence of the  
CC neural cell adhesion molecule (NCAM), its fragment, variant or its mimic,  
CC for the preparation of a medicament for preventing death of cells  
CC presenting the NCAM or an NCAM ligand. (I) is useful in the preparation  
CC of a medicament for preventing death of cells presenting the NCAM or an  
CC NCAM ligand. The medicament is for the stimulation of the survival of  
CC heart muscle cells, such as survival after acute myocardial infarction.  
CC The medicament is for the treatment of diseases or conditions of the  
CC central and peripheral nervous system, such as postoperative nerve  
CC damage, traumatic nerve damage, e.g. resulting from spinal cord injury,  
CC impaired myelination of nerve fibres, postischaemic damage, e.g.  
CC resulting from a stroke, multiinfarct dementia, multiple sclerosis, nerve  
CC degeneration associated with diabetes mellitus, neuro-muscular

CC degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease and  
CC Huntington's disease. The medicament is for the treatment of diseases or  
CC conditions of the muscles including conditions with impaired function of  
CC neuro-muscular connections, such as genetic or traumatic atrophic muscle  
CC disorders, and for the treatment of diseases of conditions of various  
CC organs, such as degenerative conditions of the gonads, pancreas (e.g.  
CC diabetes mellitus type I and II) and kidney (e.g. nephrosis). ABG69329-  
CC ABG69352 represent human NCAM peptides of the invention  
XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKE 4  
||||  
Db 1 AKKE 4

RESULT 20

AAO18039

ID AAO18039 standard; peptide; 11 AA.

XX

AC AAO18039;

XX

DT 30-AUG-2002 (first entry)

XX

DE Human immunoglobulin E epitope SEQ ID NO: 31.

XX

KW Allergy; immunoglobulin E; IgE; vaccine; immunogen; epitope; human;  
KW non-anaphylactogenic; antiallergic.

XX

OS Homo sapiens.

XX

PN WO200234288-A2.

XX

PD 02-MAY-2002.

XX

PF 24-OCT-2001; 2001WO-EP012392.

XX

PR 27-OCT-2000; 2000GB-00026334.

XX

PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX

PI Vinals Y De BassolsC;

XX

DR WPI; 2002-479702/51.

XX

PT New peptides epitopes and mimotopes derived from IgE, useful for treating  
PT or preventing allergies, for typing circulating anti-IgE, or for  
PT diagnosing atopy.

XX

PS Claim 1; Page 5; 28pp; English.

XX

CC The present invention provides peptide epitopes derived from human  
CC immunoglobulin E (IgE), which are non-anaphylactogenic and can be used as

CC immunogens to diagnose and treat allergies. The present sequence is an  
CC epitope of the invention

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ERQR 7  
|||  
Db 2 ERQR 5

RESULT 21

AAP60142

ID AAP60142 standard; peptide; 11 AA.

XX

AC AAP60142;

XX

DT 25-MAR-2003 (revised)

DT 31-OCT-2002 (revised)

DT 07-JUL-1991 (first entry)

XX

DE Type 3 pentapeptide linked to VP3 peptide suitable for use in a vaccine  
DE against a disease caused by type 3 poliovirus.

XX

KW Vaccine; diagnosis; enterovirus disease; poliovirus type 1; type 2;

KW type 3.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Region 1. .5

FT /label= type 3 pentapeptide

FT Misc-difference 1

FT /label= R,K

FT /note= "pref. R"

FT Misc-difference 2

FT /label= N,Q,D,E

FT /note= "pref. N"

FT Misc-difference 3

FT /label= see above

FT Misc-difference 5

FT /label= D,E

FT /note= "pref. D"

FT Region 6. .11

FT /label= VP3 peptide

XX

PN EP197772-A.

XX

PD 15-OCT-1986.

XX

PF 03-APR-1986; 86EP-00302481.

XX

PR 03-APR-1985; 85GB-00008685.

PR 03-APR-1986; 86GB-00008140.

XX  
PA (NATR ) NAT RES DEV CORP.  
PA (BRTE-) BRITISH TECHNOLOGY GROUP LTD.  
XX  
PI Minor PD, Evans DMA, Schild GC, Almond JW, Ferguson M;  
XX  
DR WPI; 1986-273645/42.  
XX  
PT Synthetic peptide for vaccination or diagnosis of enter-virus disease -  
PT comprises fragment coded for by polio virus type 3 Sabin strain capsid  
PT protein RNA.  
XX  
PS Disclosure; Page 15; 53pp; English.  
XX  
CC The inventors claim synthetic peptides for use in vaccination against or  
CC diagnosis of a disease caused by an enterovirus (see AAN60118). The  
CC peptides are coded for by codons 286-288 or 286-290 in the RNA sequence  
CC coding for the structural capsid protein VP1 of poliovirus type 3 Sabin  
CC strain or by equivalent codons of another enterovirus, or antigenic  
CC equivs. Also claimed are synthetic peptides comprising the above peptides  
CC linked to (a) a hexapeptide coded for by codons 93-98 as above, or (b) a  
CC peptide sequence comprising AA residues 58 and 59 of the VP3 capsid  
CC protein of an enterovirus. Typical doses are 100mg-1mg, i.m. (Updated on  
CC 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct  
CC PA field.)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10  
|||  
Db 9 KDT 11

RESULT 22  
AAP71164  
ID AAP71164 standard; protein; 11 AA.  
XX  
AC AAP71164;  
XX  
DT 25-MAR-2003 (revised)  
DT 03-OCT-2002 (revised)  
DT 04-APR-1991 (first entry)  
XX  
DE Peptide which inhibits the binding of fibrinogen to platelets.  
XX  
KW Fibrinogen; platelets; cancer; cell attachment.  
XX  
OS Synthetic.  
XX  
PN EP220957-A.  
XX  
PD 06-MAY-1987.  
XX

PF 27-OCT-1986; 86EP-00308335.  
XX  
PR 28-OCT-1985; 85US-00791872.  
XX  
PA (SCRI ) SCRIPPS CLINIC & RES FOUND.  
XX  
PI Zimmerman TS, Ruggeri ZM, Houghten R;  
XX  
DR WPI; 1987-124477/18.  
XX  
PT New peptide(s) - useful for modulating cell adhesion and inhibiting  
PT binding of adhesive proteins to blood platelets esp. in treating cancers.  
XX  
PS Claim 19; Page 7; 7pp; English.  
XX  
CC The peptide inhibits the binding of fibrinogen to platelets and inhibits  
CC the aggregation of cells or platelets to each other since it modulates  
CC cell adhesion and inhibits the binding of adhesive proteins to blood  
CC platelets. The peptide has superior activity to known peptides and has  
CC similar properties. The peptide is useful for therapeutic and diagnostic  
CC purposes, esp. for inhibiting cell-cell attachment and cell growth  
CC phenomena such as cancer. (Updated on 03-OCT-2002 to add missing OS  
CC field.) (Updated on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 6 RQR 8

RESULT 23  
AAP90643  
ID AAP90643 standard; protein; 11 AA.  
XX  
AC AAP90643;  
XX  
DT 10-MAR-2003 (revised)  
DT 09-AUG-1990 (first entry)  
XX  
DE Signal peptide NOS Synthetic.  
XX  
KW NOS; signal peptide; nucleolus.  
XX  
OS Unidentified.  
XX  
PN JP01096196-A.  
XX  
PD 14-APR-1989.  
XX  
PF 08-OCT-1987; 87JP-00252377.  
XX  
PR 08-OCT-1987; 87JP-00252377.

XX  
PA (HATA/) HATANAKA S.  
XX  
DR WPI; 1989-155085/21.  
XX  
PT New peptide NOS having specific aminoacid sequence - used to localise  
PT protein in nucleolus.  
XX  
PS Claim 1; Page 1; 12pp; Japanese.  
XX  
CC The peptide is useful for localising a protein in the nucleolus. DNA  
CC encoding it is inserted downstream of promoter in a plasmid to give pNOS  
CC Synthetic. DNA encoding an opt protein is also ligated into the vector,  
CC and the pNOS introduced to a host (eg E.coli). Plasmid DNA is then  
CC extracted from the cells and transfected into eukaryotic cells which have  
CC a nucleolus. Protein localisation can be detected immunologically within  
CC hours. See also AAP90642-4. (Updated on 10-MAR-2003 to add missing OS  
CC field.)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 6 RQR 8

RESULT 24  
AAR02183  
ID AAR02183 standard; protein; 11 AA.  
XX  
AC AAR02183;  
XX  
DT 10-MAR-2003 (revised)  
DT 02-AUG-1990 (first entry)  
XX  
DE Peptide which binds to Immunoglobulin E (IgE) receptors inhibiting IgE  
DE binding.  
XX  
KW Immunoglobulin E (IgE); anti-allergic drug; IgE binding inhibitor.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1  
FT /label= OTHER  
FT /note= "H-Ala"  
FT Misc-difference 11  
FT /label= OTHER  
FT /note= "Phe-OH"  
XX  
PN JP01299298-A.  
XX  
PD 04-DEC-1989.

XX  
PF 27-MAY-1988; 88JP-00129721.  
XX  
PR 27-MAY-1988; 88JP-00129721.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
DR WPI; 1990-019330/03.  
XX  
PT Peptides which bind to IgE receptors inhibiting IgE binding - used as  
PT antiallergic drug having no side effects.  
XX  
PS Claim 2; Page 843; 8pp; Japanese.  
XX  
CC It is the new sequence No 15 and has an anti-allergic effect. It binds to  
CC IgE receptors on cell surfaces and inhibits IgE binding to receptors. It  
CC can be used as an anti-allergic drug, having no side effects. (Updated on  
CC 10-MAR-2003 to add missing OS field.)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QRK 8  
|||  
Db 7 QRK 9

RESULT 25  
AAR06031  
ID AAR06031 standard; protein; 11 AA.  
XX  
AC AAR06031;  
XX  
DT 25-MAR-2003 (revised)  
DT 20-NOV-1990 (first entry)  
XX  
DE Oligopeptide, antigenic to N.meningitidis.  
XX  
KW Meningococcal disease; meningitis; vaccine;  
KW Class I outer membrane protein; ds.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9006696-A.  
XX  
PD 28-JUN-1990.  
XX  
PF 19-DEC-1988; 88NL-00003111.  
XX  
PR 19-DEC-1988; 88NL-00003111.  
PR 06-JAN-1989; 89NL-00000036.  
PR 26-JUN-1989; 89NL-00001612.  
XX  
PA (PRAX-) PRAXIS BILOGICS IN.

PA (VOLK-) RIJKINSINST VOLKSGEZONDH.  
PA (SEID/) SEID R C.  
PA (NEVW-) NEDERLAND VERT MIN VAN.  
XX  
PI Seid RC, Paradiso PR, Poolman JT, Hoogerhout P, Wiertz EJ;  
PI Vanderley P, Heckels JE, Clarke IN;  
XX  
DR WPI; 1990-224326/29.  
XX  
PT Meningococcus class 1 outer-membrane protein vaccine - useful to immunise  
PT against meningococcal disease.  
XX  
PS Claim 50; Page 102; 120pp; English.  
XX  
CC Peptides derived from outer membrane, encoding homo/heterologous product  
CC such as a antigen-flagelin fusion protein, are useful in eliciting a  
CC strong and wide ranging immune response against most serotypes. (Updated  
CC on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 8 KDT 10  
|||  
Db 3 KDT 5

RESULT 26  
AAR08092  
ID AAR08092 standard; protein; 11 AA.  
XX  
AC AAR08092;  
XX  
DT 25-MAR-2003 (revised)  
DT 01-MAR-1991 (first entry)  
XX  
DE Antifreeze segment #2 encoded by SS3.  
XX  
KW synthetic antifreeze polypeptide; cryopreservation;  
KW core repetitive sequence.  
XX  
OS Synthetic.  
XX  
PN WO9013571-A.  
XX  
PD 15-NOV-1990.  
XX  
PF 10-MAY-1989; 89US-00350481.  
XX  
PR 10-MAY-1989; 89US-00350481.  
PR 10-APR-1990; 90US-00507716.  
XX  
PA (DNAP ) DNA PLANT TECHN COR.  
XX

PI Warren GJ, Mueller JM, McKown RJ, Dunsmuir P;  
XX  
DR WPI; 1990-361428/48.  
XX  
PT New anti-freeze poly-peptide(s) - used for cryo-protection of e.g. foods,  
PT medically used biological(s), plant prods. or plants during growth.  
XX  
PS Disclosure; Fig 4; 11pp; English.  
XX  
CC Synthetic anti-freeze polypeptides (saf) comprise a specifically  
CC cleavable site and a region containing at least two "core" segments such  
CC as the 11mer given here. The saf's suppress ice crystal growth by binding  
CC to the growing crystal face and blocking sites for further crystal  
CC growth. They can be used to maximise retention of important properties of  
CC organic materials through freezing and thawing processes. The basic  
CC design of the polypeptides is based on known antifreeze polypeptides from  
CC insects and fish, e.g. the winter flounder. See also AAQ06649-Q06652,  
CC AAQ06656, AAQ06658, AAQ06660-Q06672, AAR08070-6, AAR08087-R08091,  
CC AAR08093. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-  
CC MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI  
CC field.)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 8 AKK 10

RESULT 27  
AAR15673  
ID AAR15673 standard; protein; 11 AA.  
XX  
AC AAR15673;  
XX  
DT 25-MAR-2003 (revised)  
DT 13-FEB-1992 (first entry)  
XX  
DE Asn-residue specific protease Asn-component.  
XX  
KW Asparagine; Asn; protease; transpeptidation; amine; DNP.  
XX  
OS Synthetic.  
XX  
PN EP458475-A.  
XX  
PD 27-NOV-1991.  
XX  
PF 30-APR-1991; 91EP-00303884.  
XX  
PR 21-MAY-1990; 90JP-00129148.  
XX  
PA (TAKI ) TAKARA SHUZO CO LTD.

XX  
PI Koyama N, Kato I, Matsushita H, Abe Y, Ishii SI;  
XX  
DR WPI; 1991-348154/48.  
XX  
PT Asparagine-residue specific protease - used as trans:peptisation reagent  
PT for the prepn. of peptide(s) esp. physiologically active peptide(s).  
XX  
PS Disclosure; Page 7; 12pp; English.  
XX  
CC This peptide is used as Asn component and GG, GGH, G-NH<sub>2</sub> or GG-NH<sub>2</sub> as the  
CC amine component. The reaction was carried out at 37 deg C for 3 hrs. with  
CC the pH 7.7. The reaction mix. was analysed by C18 reversed-phase HPLC.  
CC The transpeptidation prod. is shown in AAR15674. See also AAR15672-74.  
CC (Updated on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 8 RQR 10

RESULT 28  
AAR12168  
ID AAR12168 standard; protein; 11 AA.  
XX  
AC AAR12168;  
XX  
DT 20-AUG-1991 (first entry)  
XX  
DE Neuropeptide Y analogue #3.  
XX  
KW neuropeptide Y; NPY; antagonist.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 2  
FT /label= OTHER  
FT /note= "8-aminooctanoic acid"  
XX  
PN DE3939797-A.  
XX  
PD 06-JUN-1991.  
XX  
PF 01-DEC-1989; 89DE-03939797.  
XX  
PR 01-DEC-1989; 89DE-03939797.  
XX  
PA (BADI ) BASF AG.  
XX  
PI Zechel JC, Schult S, Unger L;

XX  
DR WPI; 1991-172223/24.  
XX  
PT New peptide(s) derived from neuro-peptide Y - are neuro-peptide Y  
PT antagonists, useful as hypotensives and in treatment of e.g. vessel  
PT spasms.  
XX  
PS Example 5; Page 5; 7pp; German.  
XX  
CC This peptide is a competitive antagonist of neuropeptide Y so is useful  
CC for treating high blood pressure and vascular spasms. It can also be used  
CC as a diagnostic/analytical reagent, e.g. for investigating biochemical or  
CC patho-physiological properties of neuropeptide Y. See also AAR12164,  
CC AAR12166-7 and AAR12169-R12175  
XX  
SQ Sequence 11 AA;  
  
Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 RQR 7  
|||  
Db 8 RQR 10  
  
RESULT 29  
AAR12171  
ID AAR12171 standard; protein; 11 AA.  
XX  
AC AAR12171;  
XX  
DT 20-AUG-1991 (first entry)  
XX  
DE Neuropeptide Y analogue #6.  
XX  
KW neuropeptide Y; NPY; antagonist.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 3  
FT /label= OTHER  
FT /note= "8-aminoctanoic acid"  
XX  
PN DE3939797-A.  
XX  
PD 06-JUN-1991.  
XX  
PF 01-DEC-1989; 89DE-03939797.  
XX  
PR 01-DEC-1989; 89DE-03939797.  
XX  
PA (BADI ) BASF AG.  
XX  
PI Zechel JC, Schult S, Unger L;  
XX

DR WPI; 1991-172223/24.

XX

PT New peptide(s) derived from neuro-peptide Y - are neuro-peptide Y antagonists, useful as hypotensives and in treatment of e.g. vessel spasms.

XX

PS Example 27; Page 6; 7pp; German.

XX

CC This peptide is a competitive antagonist of neuropeptide Y so is useful  
CC for treating high blood pressure and vascular spasms. It can also be used  
CC as a diagnostic/analytical reagent, e.g. for investigating biochemical or  
CC patho-physiological properties of neuropeptide Y. See also AAR12164,  
CC AAR12166-R12170 and AAR12172-5

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7

|||

Db 8 RQR 10

RESULT 30

AAR12173

ID AAR12173 standard; protein; 11 AA.

XX

AC AAR12173;

XX

DT 20-AUG-1991 (first entry)

XX

DE Neuropeptide Y analogue #8.

XX

KW neuropeptide Y; NPY; antagonist.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers  
FT Modified-site 1  
FT /label= p-hydroxyphenylpropionyl-Pro  
FT Misc-difference 2  
FT /label= OTHER  
FT /note= "8-aminoctanoic acid"

XX

PN DE3939797-A.

XX

PD 06-JUN-1991.

XX

PF 01-DEC-1989; 89DE-03939797.

XX

PR 01-DEC-1989; 89DE-03939797.

XX

PA (BADI ) BASF AG.

XX

PI Zechel JC, Schult S, Unger L;

XX  
DR WPI; 1991-172223/24.  
XX  
PT New peptide(s) derived from neuro-peptide Y - are neuro-peptide Y  
PT antagonists, useful as hypotensives and in treatment of e.g. vessel  
PT spasms.  
XX  
PS Example 18; Page 6; 7pp; German.  
XX  
CC This peptide is a competitive antagonist of neuropeptide Y so is useful  
CC for treating high blood pressure and vascular spasms. It can also be used  
CC as a diagnostic/analytical reagent, e.g. for investigating biochemical or  
CC patho-physiological properties of neuropeptide Y. See also AAR12164,  
CC AAR12166-R12172 and AAR12174-5  
XX  
SQ Sequence 11 AA;  
  
Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 RQR 7  
|||  
Db 8 RQR 10  
  
RESULT 31  
AAR22743  
ID AAR22743 standard; protein; 11 AA.  
XX  
AC AAR22743;  
XX  
DT 25-MAR-2003 (revised)  
DT 27-AUG-1992 (first entry)  
XX  
DE Non-A, Non-B hepatitis virus antibody binding peptide.  
XX  
KW NANBH; immunoreactive; detection.  
XX  
OS Synthetic.  
XX  
PN EP479376-A.  
XX  
PD 08-APR-1992.  
XX  
PF 05-OCT-1990; 90EP-00202658.  
XX  
PR 26-SEP-1991; 91EP-00202498.  
XX  
PA (ALKU ) AKZO NV.  
XX  
PI Habets WJA;  
XX  
DR WPI; 1992-116131/15.  
XX  
PT New peptide(s) reactive with antibodies to hepatitis non-A, non-B, virus  
PT - for detection of NANBH and its antibodies in body fluids.

XX  
PS Example; Page 7; 9pp; English.  
XX  
CC The sequence is that of a peptide which is immunoreactive with antibodies  
CC to hepatitis non-A, non-B (NANBH) virus, it was prep'd. by stepwise solid  
CC phase peptide synthesis. It can be used to detect NANBH antibodies in  
CC test fluids. It has improved immunochemical reactivity, a high affinity  
CC to NANBH antibodies and is of a safe, non-infectious origin. See also  
CC AAR22727-R22744. (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QRK 8  
|||  
Db 1 QRK 3

RESULT 32  
AAR35381  
ID AAR35381 standard; peptide; 11 AA.  
XX  
AC AAR35381;  
XX  
DT 25-MAR-2003 (revised)  
DT 07-JUN-1993 (first entry)  
XX  
DE Amphiphilic peptide #112 used to treat oral infections.  
XX  
KW Adverse oral conditions; amphipathic; anti-bacterial; anti-viral;  
KW anti-fungal; dental plaque; dental caries; periodontal disease;  
KW gingivitis; ionophore; ion-channel forming.  
XX  
OS Synthetic.  
XX  
PN WO9301723-A1.  
XX  
PD 04-FEB-1993.  
XX  
PF 09-JUL-1992; 92WO-US005757.  
XX  
PR 25-JUL-1991; 91US-00735070.  
XX  
PA (MAGA-) MAGAININ PHARM INC.  
XX  
PI Berkowitz B, Jacob L;  
XX  
DR WPI; 1993-058434/07.  
XX  
PT Peptide(s) for prophylaxis and treatment of oral disorders - used for  
PT periodontal disease, plaque, dental caries, gingivitis, etc.  
XX  
PS Claim 2; Page 129; 143pp; English.  
XX

CC This is a specific example of a highly generic formula covering preferred  
CC amphiphilic peptides for use in preventing or treating adverse oral  
CC conditions. The peptide is an ionophore (i.e. an ion- channel forming  
CC peptide) which has anti-bacterial, anti-viral, anti- fungal activity,  
CC etc. making it suitable for use in oral compositions to treat or prevent  
CC periodontal disease, plaque, dental caries, halitosis and gingivitis. The  
CC anti-bacterial action will also be useful against bacteria associated  
CC with dental implant infections and the peptides can stimulate the healing  
CC of wounds in the oral cavity. (Updated on 25-MAR-2003 to correct PN  
CC field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 1 AKK 3

RESULT 33

AAR32351

ID AAR32351 standard; peptide; 11 AA.

XX

AC AAR32351;

XX

DT 05-JUL-1993 (first entry)

XX

DE Human Factor X peptide.

XX

KW Anticoagulant; intrinsic; extrinsic; prothrombin activation; thrombin;  
KW formation; Factor Xa; pathway mediated activation; inhibition.

XX

OS Synthetic.

XX

PN US5187155-A.

XX

PD 16-FEB-1993.

XX

PF 23-JUN-1989; 89US-00371561.

XX

PR 23-JUN-1989; 89US-00371561.

XX

PA (TEXA ) UNIV TEXAS SYSTEM.

XX

PI Fair DS;

XX

DR WPI; 1993-075751/09.

XX

PT Compsns. comprising peptide(s) of 10-50 aminoacid residues - inhibit  
PT factor X activation and/or Factor Xa function, useful for preventing  
PT blood clot formation and treating deep vein thrombosis, pulmonary  
PT embolism, etc.

XX

PS Example; Page 6; 23pp; English.

XX  
CC The sequence is that of a peptide corresponding to amino acids 384-394 of  
CC the human factor X molecule which was tested for its effect, (as a % of  
CC the control rate), on the rate of Factor Xa formation and on the rate of  
CC thrombin formation. The results obtd. were for activation of Factor X by  
CC the extrinsic activation complex 100%, by the intrinsic activation  
CC complex 72%, and activation by RVV-X, 85%. For the rate of thrombin  
CC formation the rate was 100% as compared to the control rate  
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10  
|||  
Db 5 KDT 7

RESULT 34

AAR33973

ID AAR33973 standard; peptide; 11 AA.

XX

AC AAR33973;

XX

DT 25-MAR-2003 (revised)

DT 21-JUL-1993 (first entry)

XX

DE Amphiphilic peptide (e), #2.

XX

KW Hydrophobic; hydrophilic; neutral; (e); ionophore; channel-forming;  
KW human; virus; antimicrobial; antiviral; antibacterial; antitumour;  
KW antiparasitic; spermicide; preservative; sterilant; disinfectant;  
KW wound healing; burn; infection; eye; cysts; spores; trophozoites; plants;  
KW contamination.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers  
FT Modified-site 1  
FT /note= "May be acetylated"  
FT Modified-site 11  
FT /note= "May be amidated"

XX

PN WO9305802-A1.

XX

PD 01-APR-1993.

XX

PF 04-SEP-1992; 92WO-US007622.

XX

PR 13-SEP-1991; 91US-00760054.

PR 20-APR-1992; 92US-00870960.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Maloy WL, Kari UP, Williams JI;

XX  
DR WPI; 1993-117245/14.  
XX  
PT New biologically active amphiphilic peptide cpds. - having ion channel-forming properties used for inhibiting growth of target cells, virus or viral-infected cells.  
XX  
PS Claim 27; Page 33; 46pp; English.  
XX  
CC This sequence is an example of a biologically active peptide which  
CC corresponds to the generic sequence; R1-R2-R2-R1-R1-R2-R2-R1-R2-R2-R1  
CC where R1 = a hydrophobic amino acid; and R2 = a basic hydrophilic or  
CC neutral hydrophilic amino acid. This basic structure was designated (e).  
CC Peptides such as this are ionophores ie. they have channel-forming  
CC properties. The peptides can be administered to a host, eg, humans, to  
CC inhibit the growth of a target cell, virus or virally infected cell. They  
CC can be used as antimicrobial, antiviral agents, antibacterial agents,  
CC antitumour agents, antiparasitic agents, and as spermicides. They can be  
CC used as preservatives or sterilants or disinfectants. These peptides can  
CC also be used to promote or stimulate healing of wounds, to treat and/or  
CC prevent skin or burn infections, to prevent or treat eye  
CC infections and to kill cysts, spores or trophozoites of infection causing  
CC organisms. The peptides may also be administered to plants to prevent or  
CC treat microbial, viral or parasitic contamination. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 1 AKK 3

RESULT 35  
AAR31163  
ID AAR31163 standard; peptide; 11 AA.  
XX  
AC AAR31163;  
XX  
DT 25-MAR-2003 (revised)  
DT 10-MAY-1993 (first entry)  
XX  
DE C-terminal substd. amphiphilic peptide #112.  
XX  
KW ion-channel forming; ionophore; antibiotic; anti-tumour; anti-virus;  
KW wound healing.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 11  
FT /note= "Leu-(C=O)-T, T= O-R, NH-NH2, NH-OH or NR'R''; R= opt.substd. 1-10C aliphatic, aromatic or aralkyl gp.; R',

FT R''= H or from one of gps. i and ii; gp.i= 1-10C hydroxy-  
FT substd. aliphatic, aromatic or aralkyl gp.; gp.ii= amino-  
FT substd. aliphatic, aromatic, aralkyl or alkylaromatic gp.  
FT and at least one of R' and R'' = gp.i or gp.ii'''  
XX  
PN WO9222317-A1.  
XX  
PD 23-DEC-1992.  
XX  
PF 01-JUN-1992; 92WO-US004603.  
XX  
PR 12-JUN-1991; 91US-00713716.  
XX  
PA (MAGA-) MAGAININ PHARM INC.  
XX  
PI Maloy WL, Kari UP;  
XX  
DR WPI; 1993-017904/02.  
XX  
PT New C-terminal-substd. amphiphilic peptide(s) - for treating bacterial,  
PT viral or fungal infections and tumours, also useful as spermicide.  
XX  
PS Claim 21; Page 114; 124pp; English.  
XX  
CC This peptide is a preferred example of a highly generic amphiphilic  
CC peptide with a C-terminal modification which increases the peptide's  
CC biological activity c.f. the unmodified peptide. The preferred C-terminal  
CC modification is -(CO)-NHCH2CH2OH or -(CO)-NHCH2CH2NH2. Such substd.  
CC peptides may be used for inhibiting the growth of a target cell, virus or  
CC virally-infected cell in a host. The peptides have a broad range of  
CC potent antibiotic activity, e.g. against gram- negative and gram-positive  
CC bacteria, fungi, protozoa and parasites. The peptides can also be used to  
CC promote wound healing and treatment of burns. Other preferred amphiphilic  
CC peptides include magainins and their analogues, PGLa, XPF, CPF, a  
CC cecropin and a sarcotoxin. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 1 AKK 3

RESULT 36  
AAR34248  
ID AAR34248 standard; peptide; 11 AA.  
XX  
AC AAR34248;  
XX  
DT 25-MAR-2003 (revised)  
DT 04-AUG-1993 (first entry)  
XX  
DE Mutant HTLV-I residues 88-98, peptide 2L-1.2.

XX  
KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;  
KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.  
XX  
OS Synthetic.  
XX  
PN WO9306843-A1.  
XX  
PD 15-APR-1993.  
XX  
PF 08-OCT-1992; 92WO-US008405.  
XX  
PR 08-OCT-1991; 91US-00771553.  
XX  
PA (UYDU-) UNIV DUKE.  
XX  
PI Palker TJ, Haynes BF;  
XX  
DR WPI; 1993-134125/16.  
XX  
PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful  
PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.  
XX  
PS Example 7; Page 32; 50pp; English.  
XX  
CC To determine which amino acids within the HTLV-I envelope amino acids 88-  
CC 98 were required for absorption of neutralising anti-peptide antibodies  
CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which  
CC sequential amino acids were each replaced by the amino acid alanine.  
CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native  
CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93  
CC and 95 were important for HTLV-I neutralisation. See also AAR34225-57.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 2 AKK 4

RESULT 37  
AAR30442  
ID AAR30442 standard; peptide; 11 AA.  
XX  
AC AAR30442;  
XX  
DT 25-MAR-2003 (revised)  
DT 17-MAY-1993 (first entry)  
XX  
DE Synthetic sequence of glycoalbumin immunogen.  
XX  
KW V8; trypsin; glycosylation; albumin; glucose; diabetes.

XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 7  
FT /note= "in vivo glycosylated"  
XX  
PN US5173422-A.  
XX  
PD 22-DEC-1992.  
XX  
PF 03-MAY-1990; 90US-00518681.  
XX  
PR 22-AUG-1986; 86US-00899456.  
PR 02-JUN-1987; 87US-00054131.  
PR 19-FEB-1988; 88US-00158200.  
XX  
PA (MILE ) MILES INC.  
XX  
PI Knowles WJ, Marchesi VT;  
XX  
DR WPI; 1993-017567/02.  
XX  
PT Monoclonal antibody specific for human glyco-albumin - used for determinn.  
PT of extent of glycosylation of albumin in monitoring glucose level in  
PT diabetes.  
XX  
PS Disclosure; Page 14; 22pp; English.  
XX  
CC The sequence shows a preferred synthetic glycosylated peptide from  
CC glycoalbumin. The peptide can be linked to a conventional immunogenic  
CC carrier material to form an immunogen. The immunogen may be used to raise  
CC monoclonal antibodies which are useful for the detection of the  
CC glycosylated form of albumin in human blood samples. This serves as a  
CC useful index of glucose level control in diabetics. See also AAR30460-71,  
CC AAR30439-47, AAR30478-9, and AAR31165-78. (Updated on 25-MAR-2003 to  
CC correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 ERQ 6  
|||  
Db 2 ERQ 4

RESULT 38  
AAR30463  
ID AAR30463 standard; peptide; 11 AA.  
XX  
AC AAR30463;  
XX  
DT 25-MAR-2003 (revised)  
DT 17-MAY-1993 (first entry)

XX  
DE Synthetic sequence of glycoalbumin in the region of lysine 525.  
XX  
KW V8; trypsin; glycosylation; albumin; glucose; diabetes.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 7  
FT /note= "corresponds to lysine 525 and is in vivo  
FT glycosylated"  
XX  
PN US5173422-A.  
XX  
PD 22-DEC-1992.  
XX  
PF 03-MAY-1990; 90US-00518681.  
XX  
PR 22-AUG-1986; 86US-00899456.  
PR 02-JUN-1987; 87US-00054131.  
PR 19-FEB-1988; 88US-00158200.  
XX  
PA (MILE ) MILES INC.  
XX  
PI Knowles WJ, Marchesi VT;  
XX  
DR WPI; 1993-017567/02.  
XX  
PT Monoclonal antibody specific for human glyco-albumin - used for determinn.  
PT of extent of glycosylation of albumin in monitoring glucose level in  
PT diabetes.  
XX  
PS Disclosure; Fig 1; 22pp; English.  
XX  
CC The sequence shows a preferred synthetic glycosylated peptide from  
CC glycoalbumin in the region of lysine 525. The peptide can be linked to a  
CC conventional immunogenic carrier material to form an immunogen. The  
CC immunogen may be used to raise monoclonal antibodies which are useful for  
CC the detection of the glycosylated form of albumin in human blood samples.  
CC This serves as a useful index of glucose level control in diabetics. See  
CC also AAR30460-71, AAR30439-47, AAR30478-9, and AAR31165-78. (Updated on  
CC 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR  
CC field.)  
XX  
SQ Sequence 11 AA;  
  
Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 4 ERQ 6  
|||  
Db 2 ERQ 4

RESULT 39  
AAR30478

ID AAR30478 standard; peptide; 11 AA.  
XX  
AC AAR30478;  
XX  
DT 25-MAR-2003 (revised)  
DT 17-MAY-1993 (first entry)  
XX  
DE Synthetic sequence of glycoalbumin immunogen.  
XX  
KW V8; trypsin; glycosylation; albumin; glucose; diabetes.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 7  
FT /note= "in vivo glycosylated"  
XX  
PN US5173422-A.  
XX  
PD 22-DEC-1992.  
XX  
PF 03-MAY-1990; 90US-00518681.  
XX  
PR 22-AUG-1986; 86US-00899456.  
PR 02-JUN-1987; 87US-00054131.  
PR 19-FEB-1988; 88US-00158200.  
XX  
PA (MILE ) MILES INC.  
XX  
PI Knowles WJ, Marchesi VT;  
XX  
DR WPI; 1993-017567/02.  
XX  
PT Monoclonal antibody specific for human glyco-albumin - used for determin.  
PT of extent of glycosylation of albumin in monitoring glucose level in  
PT diabetes.  
XX  
PS Disclosure; Page 12; 22pp; English.  
XX  
CC The sequence shows a preferred synthetic glycosylated peptide from  
CC glycoalbumin. The peptide can be linked to a conventional immunogenic  
CC carrier material to form an immunogen. The immunogen may be used to raise  
CC monoclonal antibodies which are useful for the detection of the  
CC glycosylated form of albumin in human blood samples. This serves as a  
CC useful index of glucose level control in diabetics. See also AAR30460-71,  
CC AAR30439-47, AAR30479, and AAR31165-78. (Updated on 25-MAR-2003 to  
CC correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)  
XX  
SQ Sequence 11 AA;  
  
Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 4 ERQ 6  
|||  
Db 2 ERQ 4

RESULT 40  
AAR41495  
ID AAR41495 standard; peptide; 11 AA.  
XX  
AC AAR41495;  
XX  
DT 23-FEB-1994 (first entry)  
XX  
DE TNF inhibitory peptide VII.  
XX  
KW Tumour necrosis factor; TNF; inhibition; solid phase synthesis; ss.  
XX  
OS Synthetic.  
XX  
PN JP05194594-A.  
XX  
PD 03-AUG-1993.  
XX  
PF 21-JAN-1992; 92JP-00029044.  
XX  
PR 21-JAN-1992; 92JP-00029044.  
XX  
PA (SAGA.) SAGAMI CHEM RES CENTRE.  
XX  
DR WPI; 1993-282916/36.  
XX

PT TNF inhibitory novel peptide(s) - include N-terminal amino Gp. which is  
PT opt. modified with acetyl, T-butoxycarbonyl or benzyl-oxy-carbonyl Gp.  
PT and C-terminal carboxy Gp. is opt. amidated.

XX  
PS Claim 1; Page 6; 8pp; Japanese.

CC The sequences given in AAR41489-99 are tumour necrosis factor (TNF)  
CC inhibitory peptides. They may optionally be modified at the N- terminal  
CC with an acetyl, t-butoxycarbonyl or benzylloxycarbonyl, and at the C-  
CC terminal they are optionally amidated. These peptides are produced by  
CC solid phase synthesis methods and may be produced at low cost

XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 3 AKK 5

RESULT 41  
AAR39369  
ID AAR39369 standard; peptide; 11 AA.  
XX  
AC AAR39369;  
XX

DT 25-MAR-2003 (revised)  
DT 07-DEC-1993 (first entry)  
XX  
DE Human glycoalbumin peptide ALB C11L.  
XX  
KW glycosylated albumin; immunogen; diabetes; diagnosis;  
KW monoclonal antibody.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1  
FT /note= "enables specific coupling of the peptide to  
FT immunogenic carrier"  
FT Modified-site 6  
FT /note= "potential site of further glycosylation during  
FT synthesis"  
FT Modified-site 7  
FT /note= "glycosylated Lys525"  
XX  
PN US5225354-A.  
XX  
PD 06-JUL-1993.  
XX  
PF 21-AUG-1992; 92US-00934085.  
XX  
PR 22-AUG-1986; 86US-00899456.  
PR 02-JUN-1987; 87US-00054131.  
PR 19-FEB-1988; 88US-00158200.  
PR 03-MAY-1990; 90US-00518681.  
XX  
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.  
XX  
PI Knowles WJ, Marchesi VT;  
XX  
DR WPI; 1993-226613/28.  
XX  
PT Immunoassay for glycosylated albumin in blood - using monoclonal antibody  
PT which binds specifically to human albumin glycosylated at lysine residue  
PT 525.  
XX  
PS Claim 10; Fig 1; 22pp; English.  
XX  
CC Novel monoclonal antibodies are specific for glycosylated human albumin  
CC in the region around Lys(525). Antibodies are pref. raised against  
CC peptides having the sequence Lys(519)-Glu(531), or their N- and/or C-  
CC terminal deletions, provided Lys(525) is present. Additional Tyr and/or  
CC Cys residues are opt. present at one or both peptide termini. The  
CC determination of the extent of glycosylation of albumin in an  
CC individual's blood provides a useful index of glucose level control in  
CC diabetics. (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERQ 6  
|||  
Db 2 ERQ 4

RESULT 42

AAR45132

ID AAR45132 standard; peptide; 11 AA.

XX

AC AAR45132;

XX

DT 25-MAR-2003 (revised)

DT 28-JUN-1994 (first entry)

XX

DE Amphiphilic peptide for N-terminal lipophilic substitution.

XX

KW Ion channel; magainin; PGLa; XPF; CPF; cecropin; sarcotoxin; amphiphilic;

KW hydrophobic; hydrophilic; lipophilic; growth; inhibition; target cell;

KW virus; virally-infected cell; antimicrobial; antiviral; antitumour;

KW antiparasitic; spermicide; wound healing; burn; infection.

XX

OS Synthetic.

XX

PN WO9324138-A1.

XX

PD 09-DEC-1993.

XX

PF 27-MAY-1993; 93WO-US005192.

XX

PR 01-JUN-1992; 92US-00891201.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Kari U;

XX

DR WPI; 1993-405419/50.

XX

PT Peptide(s) or proteins with an N-terminal lipophilic substit. - used for  
PT inhibiting growth of target cell, virus or virally-infected cell.

XX

PS Disclosure; Page 97-103; 113pp; English.

XX

CC A novel compsn. for inhibiting growth of a target cell, virus or virally-  
CC infected cell comprises a peptide of formula T-N(W)-X (I). X is a  
CC biologically active amphiphilic ion channel-forming peptide or protein;  
CC pref. a magainin peptide, a PGLa peptide, a XPF peptide, a CPF peptide, a  
CC cecropin or a sarcotoxin. N is the nitrogen of the N-terminal amino  
CC group. T is a lipophilic moiety; pref. R-CO, where R is a 2-16C  
CC hydrocarbon (alkyl or aromatic or alkylaromatic). T is pref. an octanoyl  
CC group. W is T or hydrogen. Amphiphilic peptides as examples of X are  
CC given in AAR45115-138. The N-terminal subst. peptides and proteins have  
CC increased biological activity as compared with unsubstd. peptides or  
CC proteins or peptides subst. at the N-terminal with an acetyl gp. They  
CC can be used as antimicrobial agents, antiviral agents, antitumour agents,  
CC antiparasitic agents or spermicides and can also exhibit other bioactive  
CC functions. They can also be used in promoting or stimulating wound

CC healing, for the treatment of external burns and to treat and/or prevent  
CC skin and burn infections or eye infections. (Updated on 25-MAR-2003 to  
CC correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 1 AKK 3

RESULT 43

AAR34421

ID AAR34421 standard; peptide; 11 AA.

XX

AC AAR34421;

XX

DT 25-MAR-2003 (revised)

DT 05-AUG-1993 (first entry)

XX

DE Hepatitis C Ab detection peptide #5.

XX

KW Test reagent; dectection; antibody; hepatitis C; virus; HCV; epitope;  
KW structural region; diagnosis; ss.

XX

OS Synthetic.

XX

PN WO9307488-A1.

XX

PD 15-APR-1993.

XX

PF 02-OCT-1992; 92WO-JP001276.

XX

PR 02-OCT-1991; 91JP-00255524.

PR 26-MAR-1992; 92JP-00068695.

XX

PA (EIKE ) EIKEN KAGAKU KK.

PA (OSAU ) UNIV OSAKA.

PA (TANA ) TANABE SEIYAKU CO.

XX

PI Ishibashi K, Ito M, Yoshida I, Takamizawa A, Shibatani T;

XX

DR WPI; 1993-134624/16.

XX

PT Reagent for detecting antibodies to hepatitis C virus - comprises  
PT peptide(s) with the same sequence as an epitope of an HCV structural  
PT region.

XX

PS Disclosure; Page 43; 51pp; Japanese.

XX

CC The sequences given in AAR34417-25 are peptides which can be used in a  
CC test reagent for the dectection of antibodies against hepatitis C. The  
CC peptides represent epitopes of an HCV structural region and they react

CC specifically with antibodies against the HCV structural region. Detection  
CC is sensitive and accurate and allows diagnosis of the infection at a  
CC very early stage. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 6 QRK 8  
    |||  
Db 1 QRK 3

RESULT 44  
AAR55163  
ID AAR55163 standard; protein; 11 AA.  
XX  
AC AAR55163;  
XX  
DT 25-MAR-2003 (revised)  
DT 11-JAN-1995 (first entry)  
XX  
DE Fragment of retinoic acid receptor RAR-beta.  
XX  
KW Liver; hap; retinoic acid receptor; steroid; thyroid; hormone; hepatoma;  
KW retinoid; antibody.  
XX  
OS Homo sapiens.  
XX  
PN US5317090-A.  
XX  
PD 31-MAY-1994.  
XX  
PF 11-DEC-1992; 92US-00989902.  
XX  
PR 16-DEC-1987; 87US-00133687.  
PR 17-DEC-1987; 87US-00134130.  
PR 20-JUN-1988; 88US-00209009.  
PR 30-NOV-1988; 88US-00278136.  
PR 30-MAR-1989; 89US-00330405.  
PR 21-AUG-1991; 91US-00751612.  
PR 30-MAR-1992; 92US-00860577.  
XX  
PA (INSP ) INST PASTEUR.  
XX  
PI Marchio A, Chambon P, Petkovich M, Krust A, Dejean A, Tiollais P;  
PI Brand N, De The HB;  
XX  
DR WPI; 1994-176333/21.  
XX  
PT Antibody specific for retinoic acid receptor-beta - useful for detecting,  
PT quantifying and identifying agonists and antagonists of retinoid  
PT activity.  
XX  
PS Claim 4; Col 40; 35pp; English.

XX  
CC The retinoic acid receptor RAR-beta is encoded by a gene designated hap.  
CC The hap gene is transcribed at low level in most human tissues, but the  
CC gene is overexpressed in prostate and kidney. Six out of seven hepatoma or  
CC hepatoma-derived cell lines express a small hap transcript which is  
CC undetectable in normal adult and foetal livers but present in all non-  
CC hepatic tissues tested. (Updated on 25-MAR-2003 to correct PF field.)  
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4  
|||  
Db 7 KKE 9

RESULT 45

AAR50563

ID AAR50563 standard; peptide; 11 AA.

XX

AC AAR50563;

XX

DT 25-MAR-2003 (revised)

DT 18-OCT-1994 (first entry)

XX

DE Amphiphilic peptide #112.

XX

KW Amphiphilic; ion forming; gynaecological malignancy; magainin; PGLa; XPF;  
KW CPF; cecropin; sarcotoxin; melittin; apidaecin; defensin;  
KW major basic protein; eosinophils; uterine; cervical; cancer;  
KW bacterial permeability increasing protein; ovarian; stage IC.

XX

OS Synthetic.

XX

PN WO9405313-A1.

XX

PD 17-MAR-1994.

XX

PF 16-AUG-1993; 93WO-US007798.

XX

PR 31-AUG-1992; 92US-00937462.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Jacob LS, Maloy WL, Baker MA;

XX

DR WPI; 1994-100851/12.

XX

PT Treating gynaecological tumours with amphiphilic peptide(s) - which form  
PT ion channels, e.g. magainin or PGLa peptide(s), partic. for treating  
PT ovarian, uterine or cervical cancers.

XX

PS Disclosure; Page 116; 130pp; English.

XX

CC The sequences given in AAR50452-568 represent amphiphilic, ion forming  
CC peptides which may be used to treat gynaecological malignancy. These  
CC peptides are based on magainin, PGLa, XPF or CPF, a cecropin, a  
CC sarcotoxin, melittin, an apidaecin, a defensin, major basic protein of  
CC eosinophils or a bacterial permeability increasing protein. These  
CC peptides are esp. used to treat ovarian, esp. stage IC, uterine or  
CC cervical cancers. (Updated on 25-MAR-2003 to correct PN field.)  
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
|||  
Db 1 AKK 3

RESULT 46

AAR55987

ID AAR55987 standard; peptide; 11 AA.

XX

AC AAR55987;

XX

DT 25-MAR-2003 (revised)

DT 19-DEC-1994 (first entry)

XX

DE Ion channel forming peptide.

XX

KW Ion channel forming peptide; tumour; skin disease; malignancy; melanoma;  
KW carcinoma; basal cell; squamous cell; magainin; PGLa; CPF peptides;  
KW cercopins; sarcotoxin; mellitin; apidocin; defensins;  
KW major basic protein; bacteria-permeability increasing protein; perforin.

XX

OS Synthetic.

XX

PN WO9412206-A1.

XX

PD 09-JUN-1994.

XX

PF 03-DEC-1993; 93WO-US011885.

XX

PR 03-DEC-1992; 92US-00984957.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Jacob LS, Maloy WL;

XX

DR WPI; 1994-199965/24.

XX

PT Treating skin cancer with ion channel forming peptide(s) - e.g.

PT magainins, mellitin etc., specifically for treating melanoma.

XX

PS Disclosure; Page 121; 136pp; English.

XX

CC The peptide is used to treat dermatological malignancies. It may be used

CC to treat especially melanoma but also basal cell and squamous cell  
CC carcinomas. It can be used together with an ion which also  
CC inhibits/prevents growth of the target cell. Peptides used for such  
CC therapy include magainin, PGLa or CPF peptides; cercopins, sarcotoxins,  
CC mellitin, apidocins, defensins, major basic protein of eosinophils;  
CC bacteria-permeability increasing protein and perforin. See also AAQ55876-  
CC Q55997. (Updated on 25-MAR-2003 to correct PN field.)  
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
|||  
Db 1 AKK 3

RESULT 47

AAR59065

ID AAR59065 standard; peptide; 11 AA.

XX

AC AAR59065;

XX

DT 25-MAR-2003 (revised)

DT 21-APR-1995 (first entry)

XX

DE Cancer treating, amphiphilic ion-channel forming peptide.

XX

KW Amphiphilic ion-channel forming peptide; cancer treatment;  
KW protease inhibitors.

XX

OS Synthetic.

XX

PN WO9419369-A1.

XX

PD 01-SEP-1994.

XX

PF 22-FEB-1994; 94WO-US002121.

XX

PR 26-FEB-1993; 93US-00021607.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Herlyn M, Jacob LS, Maloy WL;

XX

DR WPI; 1994-294258/36.

XX

PT Treating cancerous growths - by administering biologically active  
PT peptide(s) and protease inhibitors.

XX

PS Claim 2; Page 106; 124pp; English.

XX

CC AAR59060 to AAR59066 are a group of amphiphilic ion-channel forming  
CC peptides conforming to the same generic sequence. Used in combination  
CC with one or more protease inhibitors and other amphiphilic ion-channel

CC forming peptides or proteins; they are effective in the treatment of  
CC cancerous growths. In particular during surgery and radiation treatment  
CC they may be useful in inhibiting, preventing and/or destroying potential  
CC "loose" malignant cells capable of colonising other sites. (Updated on 25  
CC -MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 1 AKK 3

RESULT 48

AAR56948

ID AAR56948 standard; peptide; 11 AA.

XX

AC AAR56948;

XX

DT 25-MAR-2003 (revised)

DT 17-MAR-1995 (first entry)

XX

DE Peptide which neutralises bacterial endotoxin.

XX

KW septic shock; bacterial endotoxin; lipopolysaccharide; LPS;  
KW gram negative bacteria; conjugate moiety; septicemia; neutralising;  
KW longer activity; polyvinylpyrrolidone; dextran; hetastarch;  
KW polyvinyl alcohol; ion-channel forming; amphiphilic.

XX

OS Synthetic.

XX

PN WO9413697-A1.

XX

PD 23-JUN-1994.

XX

PF 06-DEC-1993; 93WO-US011841.

XX

PR 07-DEC-1992; 92US-00987443.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Hendi M, Rao M, Williams TJ;

XX

DR WPI; 1994-217804/26.

XX

PT New conjugates of bioactive amphiphilic peptide(s) and conjugate moiety -  
PT are useful for treatment of septic shock.

XX

PS Disclosure; Page 115; 141pp; English.

XX

CC Septic shock is often due to the body's reaction to foreign  
CC lipopolysaccharide (LPS). The compounds of the invention neutralise  
CC bacterial endotoxins without neutralising essential proteins in the

CC plasma of patients, eg.heparins. They also have longer duration of  
CC activity than unconjugated peptides. In general peptides such as this are  
CC ion-channel forming peptides.The compounds are biologically active  
CC peptides linked to a conjugate moiety, eg. carbohydrates, proteins,  
CC polyvinylpyrrolidone, polyalkylene glycols and polyvinyl alcohols. The  
CC conjugate moiety may be linked at the C- or N-terminal or internally of  
CC the peptide. AAR55591-631 and AAR56879-957 are examples of these peptide-  
CC conjugate moiety compounds (Updated on 25-MAR-2003 to correct PN field.)  
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
|||  
Db 1 AKK 3

RESULT 49

AAR50448

ID AAR50448 standard; peptide; 11 AA.

XX

AC AAR50448;

XX

DT 25-MAR-2003 (revised)

DT 17-OCT-1994 (first entry)

XX

DE Amphiphilic peptide #113.

XX

KW Amphiphilic peptide; aprotic organic solvent; alcohol; antitumour;  
KW antibiotic; antimicrobial; antifungal; antiparasitic; anticancer;  
KW antiviral; human; animal; plant; ion-channel; forming peptide.

XX

OS Synthetic.

XX

PN WO9405308-A1.

XX

PD 17-MAR-1994.

XX

PF 13-AUG-1993; 93WO-US007694.

XX

PR 28-AUG-1992; 92US-00936504.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Williams JI;

XX

DR WPI; 1994-100846/12.

XX

PT Purifying amphiphilic protein or peptide by solvent extrn. - partic. for  
PT recombinant, ion-channel forming peptide(s) such as magainins, avoids use  
PT of chaotropic agents.

XX

PS Disclosure; Page 124; 135pp; English.

XX

CC The sequences given in AAR50336-451 are amphiphilic peptides which were  
CC isolated by the method of the invention. A material containing  
CC amphiphilic peptides such as these, was treated with a mixt. of aprotic  
CC organic solvent and alcohol to form a single miscible solution. This  
CC solution was then treated with a aqueous solution to form an aqueous  
CC phase solution containing the peptides and an organic solvent phase, and  
CC the peptides were isolated from the aqueous phase. The isolated peptides  
CC may be useful as antibiotic, antimicrobial, antifungal, antiparasitic,  
CC antitumour, anticancer, and/or antiviral agents for treatment of humans,  
CC animals or plants. These peptides are esp. ion-channel forming peptides  
CC which enable biologically active ions to enter cells. (Updated on 25-MAR-  
CC 2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 1 AKK 3

RESULT 50

AAR51276

ID AAR51276 standard; protein; 11 AA.

XX

AC AAR51276;

XX

DT 25-MAR-2003 (revised)

DT 09-SEP-1994 (first entry)

XX

DE Meningococcal OMP P1.16 epitope.

XX

KW Neisseria meningitidis; meningococcus; outer membrane protein; OMP;

KW outer membrane vesicle; lipopolysaccharide; vaccine.

XX

OS Synthetic.

XX

PN WO9408021-A1.

XX

PD 14-APR-1994.

XX

PF 30-JUL-1993; 93WO-NL000163.

XX

PR 02-OCT-1992; 92NL-00001716.

XX

PA (NEWE-) NEDERLANDEN MIN WELZIJN.

XX

PI Van Der Ley PA, Poolman JT, Hoogerhout P;

XX

DR WPI; 1994-135585/16.

DR N-PSDB; AAQ62053.

XX

PT New B cell activating molecules from meningococcal lipo:polysaccharide -  
PT and derived peptide conjugates, outer membrane vesicles etc. useful in

PT vaccines effective against several meningococcal immunotypes.  
XX  
PS Example; Page 25; 62pp; English.  
XX  
CC An oligonucleotide with KpnI sticky ends (AAQ62053) encodes the P1.16  
CC epitope of *Neisseria meningitidis* outer membrane protein (OMP). The 3'  
CC end of the antisense strand overhangs the 5' end of the sense strand by 4  
CC bases, and the 3' end of the sense strand overhangs the 5' end of the  
CC antisense strand by 4 bases. Eptiopes encoded by the sense and antisense  
CC strands are given in AAR51276 and AAR55835, respectively. The  
CC oligonucleotide was placed in loop 6 of the class I OMP gene, providing a  
CC new meningococcal strain with an extra epitope for use in vaccines.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10  
|||  
Db 3 KDT 5

RESULT 51  
AAR51277  
ID AAR51277 standard; protein; 11 AA.  
XX  
AC AAR51277;  
XX  
DT 25-MAR-2003 (revised)  
DT 09-SEP-1994 (first entry)  
XX  
DE Meningococcal OMP P1.16 epitope.  
XX  
KW *Neisseria meningitidis*; meningococcus; outer membrane protein; OMP;  
KW outer membrane vesicle; lipopolysaccharide; vaccine.  
XX  
OS Synthetic.  
XX  
PN WO9408021-A1.  
XX  
PD 14-APR-1994.  
XX  
PF 30-JUL-1993; 93WO-NL000163.  
XX  
PR 02-OCT-1992; 92NL-00001716.  
XX  
PA (NEWE-) NEDERLANDEN MIN WELZIJN.  
XX  
PI Van Der Ley PA, Poolman JT, Hoogerhout P;  
XX  
DR WPI; 1994-135585/16.  
DR N-PSDB; AAQ62054.  
XX  
PT New B cell activating molecules from meningococcal lipo:polysaccharide -

PT and derived peptide conjugates, outer membrane vesicles etc. useful in  
PT vaccines effective against several meningococcal immunotypes.

XX

PS Example; Page 26; 62pp; English.

XX

CC An oligonucleotide with SpeI sticky ends (AAQ62054) encodes the P1.16  
CC epitope of *Neisseria meningitidis* outer membrane protein (OMP). The 3'  
CC end of the antisense strand overhangs the 5' end of the sense strand by 4  
CC bases, and the 3' end of the sense strand overhangs the 5' end of the  
CC antisense strand by 4 bases. Eptiopes encoded by the sense and antisense  
CC strands are given in AAR51277 and AAR55836, respectively. The  
CC oligonucleotide was placed in loop 5 of the class I OMP gene, providing a  
CC new meningococcal strain with an extra epitope for use in vaccines.  
CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10

|||

Db 3 KDT 5

RESULT 52

AAR82678

ID AAR82678 standard; protein; 11 AA.

XX

AC AAR82678;

XX

DT 23-JAN-1996 (first entry)

XX

DE V8 fragment of CD45 associating protein pp32.

XX

KW CD45; immune system; disease; pp32; T-lymphocyte; T-cell; activation;  
KW isoform; CD2; phorbol ester; identification; screening;  
KW monoclonal antibody.

XX

OS Homo sapiens.

XX

PN WO9521916-A2.

XX

PD 17-AUG-1995.

XX

PF 09-FEB-1995; 95WO-US001618.

XX

PR 14-FEB-1994; 94US-00197793.

XX

PA (BADI ) BASF AG.

XX

PI Schoenhaut D, Ratnofsky S, Meuer S, Schraven B;

XX

DR WPI; 1995-293118/38.

DR N-PSDB; AAT03910.

XX

PT Nucleic acid encoding a human pp32 protein which associates with CD45 -  
PT useful for treatment of immune system diseases and in the identification  
PT of T cell activation inhibitors.

XX

PS Example 9; Page 25; 49pp; English.

XX

CC pp32 is specifically associated with, and is a potential substrate of  
CC CD45. pp32 is constitutively phosphorylated on serine in resting T-  
CC cells. In such cells it exists in two isoforms, pp32 low and pp32 high.  
CC Both isoforms show rapid changes during T-cell activation. These changes  
CC take place within five minutes after stimulation of T- lymphocytes with  
CC monoclonal antibodies specific for CD2 or with Phorbol esters. pp32 is  
CC useful for treating diseases of the immune system and to identify  
CC inhibitors of T-cell activation. Peptide fragments of pp32 (AAR82673-81)  
CC were used to produce degenerate primers (AAT03911-19) which were then  
CC used to produce a probe to isolate a full length pp32 cDNA clone

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ERQ 6  
|||  
Db 9 ERQ 11

RESULT 53

AAW21496

ID AAW21496 standard; peptide; 11 AA.

XX

AC AAW21496;

XX

DT 16-OCT-2003 (revised)

DT 30-JUL-1997 (first entry)

XX

DE Hepatitis delta antigen derived signal oligopeptide #1.

XX

KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;  
KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;  
KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;  
KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;  
KW gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin;  
KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;  
KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;  
KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;  
KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;  
KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;  
KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.

XX

OS Hepatitis D virus.

XX

PN WO9519568-A1.

XX

PD 20-JUL-1995.

XX

PF 12-JAN-1995; 95WO-US000575.  
XX  
PR 14-JAN-1994; 94US-00182248.  
XX  
PA (RATH/) RATH M.  
XX  
PI Rath M;  
XX  
DR WPI; 1995-263953/34.  
XX  
PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as  
PT regions of max. hydrophilicity, used in modulating communication between  
PT protein(s).  
XX  
PS Claim 5; Page 72; 88pp; English.  
XX  
CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-  
CC peptides. These signal oligopeptides are localised on the surface of the  
CC protein and are represented by the hydrophilicity maxima of the protein.  
CC These peptides are enriched in charged amino acids arranged with neutral  
CC spacer amino acids. The specific signal character of these oligopeptides  
CC is determined by a characteristic combination of conformation and charge  
CC within the signal sequence. These oligopeptides may be used as vaccines  
CC in the treatment of human disease, as competitive inhibitors to prevent  
CC or reduce the metabolic action or interaction of a selected protein by  
CC blocking its specific signal sequences, or as therapeutic agents to  
CC function as feedback regulators to reduce synthesis rate of a selected  
CC protein. These peptides may be modified by omitting one or more amino  
CC acids at the N- and/or C-terminal, by substituting one or more amino  
CC acids without consideration of charge and polarity, by substituting one  
CC or more amino acids with amino acid residues with similar charge and/or  
CC polarity, by omitting one or more amino acids or a combination of these.  
CC (Updated on 16-OCT-2003 to standardise OS field)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKD 9  
|||  
Db 3 RKD 5

RESULT 54  
AAW21220  
ID AAW21220 standard; peptide; 11 AA.  
XX  
AC AAW21220;  
XX  
DT 29-JUL-1997 (first entry)  
XX  
DE Farnesyl synthetase derived signal oligopeptide #20.  
XX  
KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;  
KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;

KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;  
KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;  
KW gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin;  
KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;  
KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;  
KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;  
KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;  
KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;  
KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.  
XX

OS Homo sapiens.

XX

PN WO9519568-A1.

XX

PD 20-JUL-1995.

XX

PF 12-JAN-1995; 95WO-US000575.

XX

PR 14-JAN-1994; 94US-00182248.

XX

PA (RATH/) RATH M.

XX

PI Rath M;

XX

DR WPI; 1995-263953/34.

XX

PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as  
PT regions of max. hydrophilicity, used in modulating communication between  
PT protein(s).

XX

PS Claim 5; Page 26; 88pp; English.

XX

CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-  
CC peptides. These signal oligopeptides are localised on the surface of the  
CC protein and are represented by the hydrophilicity maxima of the protein.  
CC These peptides are enriched in charged amino acids arranged with neutral  
CC spacer amino acids. The specific signal character of these oligopeptides  
CC is determined by a characteristic combination of conformation and charge  
CC within the signal sequence. These oligopeptides may be used as vaccines  
CC in the treatment of human disease, as competitive inhibitors to prevent  
CC or reduce the metabolic action or interaction of a selected protein by  
CC blocking its specific signal sequences, or as therapeutic agents to  
CC function as feedback regulators to reduce synthesis rate of a selected  
CC protein. These peptides may be modified by omitting one or more amino  
CC acids at the N- and/or C-terminal, by substituting one or more amino  
CC acids without consideration of charge and polarity, by substituting one  
CC or more amino acids with amino acid residues with similar charge and/or  
CC polarity, by omitting one or more amino acids or a combination of these

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3

|||

RESULT 55

AAR76917

ID AAR76917 standard; peptide; 11 AA.

XX

AC AAR76917;

XX

DT 08-MAR-1996 (first entry)

XX

DE Thymosin alpha-1 peptide analogue #23.

XX

KW Thymosin alpha-1; analogue; immune system modulator; alpha-interferon;  
KW gamma-interferon; macrophage migration inhibitory factor; T-cell marker;  
KW interleukin-2 receptor; helper T-cell; solid phase synthesis;  
KW immunodeficiency; therapy; AIDS; HIV; immunodepravation.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 11

FT /note= "optionally amidated Pro or amidated Gly"

XX

PN WO9520602-A2.

XX

PD 03-AUG-1995.

XX

PF 18-JAN-1995; 95WO-US000617.

XX

PR 28-JAN-1994; 94US-00188232.

XX

PA (ALPH-) ALPHA 1 BIOMEDICALS INC.

XX

PI Wang S;

XX

DR WPI; 1995-275412/36.

XX

PT New thymosin alpha-1 peptide analogues - for the treatment of  
PT immunodeficiency diseases and the reconstitution of immune functions in  
PT immuno-depressed patients.

XX

PS Claim 7; Page ?; 24pp; English.

XX

CC The sequences represented by AAR76895-R76935 are thymosin alpha-1  
CC analogues. Thymosin alpha-1 is an immune system modulator. Thymosin alpha  
CC -1 activity includes, stimulation of alpha- and gamma-interferon  
CC production, increasing macrophage migration inhibitory factor production,  
CC inducing expression of T-cell markers (including interleukin-2  
CC receptors), and improving helper T-cell activity. These sequences  
CC function like natural thymosin alpha-1, and are easy to produce. These  
CC sequences were synthesised by solid phase synthesis on a 4-  
CC methylbenzhydrylamine resin. The peptides were cleaved from this resin  
CC using trifluoromethane sulfonic acid (TFS). These sequences can be used  
CC to reconstitute immune functions in immunodeprived and immunodepressed  
CC patients. They can also be used in the treatment of immunodeficiency  
CC diseases

XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4  
|||  
Db 1 KKE 3

RESULT 56  
AAR84537  
ID AAR84537 standard; peptide; 11 AA.  
XX  
AC AAR84537;  
XX  
DT 06-JUN-1996 (first entry)  
XX  
DE Hepatitis C virus core antigen (amino acids 8-18).  
XX  
KW Tailor-made; antigen/antibody specificity exchanger; HIV infection;  
KW heavy chain; complementarity determining region; CDR;  
KW human immunodeficiency virus; variable loop 3 domain; redirecting;  
KW epitope; HCV; hepatitis C virus; core protein.  
XX  
OS Synthetic.  
XX  
PN WO9529938-A1.  
XX  
PD 09-NOV-1995.  
XX  
PF 27-APR-1995; 95WO-SE000468.  
XX  
PR 28-APR-1994; 94SE-00001460.  
XX  
PA (FERR ) FERRING AB.  
XX  
PI Saellberg M;  
XX  
DR WPI; 1995-393040/50.  
XX  
PT Antigen-antibody specificity exchanger - used in a method to redirect a  
PT patients antibodies against polio:virus to fight HIV infection in the  
PT patient.  
XX  
PS Claim 7; Page 35; 38pp; English.  
XX  
CC An antigen/antibody specificity exchanger comprises an antibody- derived  
CC amino acid sequence (A) which specifically binds to a particular antigen,  
CC linked to an amino acid sequence (C) to which a particular antibody  
CC binds. The present sequence is a preferred example of a type (C) sequence  
CC ; it is an epitope from hepatitis C virus. Preferred type (A) sequences  
CC are complementarity determining regions from e.g. anti-HIV-1 antibodies.  
CC The specificity exchanger can redirect antibodies already present in a  
CC patient and raised against a particular antigen, to fight a different

CC antigen. For example, it was shown that anti-poliovirus antibodies could  
CC be redirected to fight HIV  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QRK 8  
|||  
Db 1 QRK 3

RESULT 57  
AAR90259  
ID AAR90259 standard; peptide; 11 AA.  
XX  
AC AAR90259;  
XX  
DT 10-JUL-1996 (first entry)  
XX  
DE Ion-channel forming peptide #111 with lipophilic N-terminal group.  
XX  
KW Ion channel forming peptide; lipophilic; N-terminal modification;  
KW magainin; inhibition; cell growth; viral replication; ionophore;  
KW membrane permeability; antimicrobial; anti-bacterial; antibiotic;  
KW anti-fungal; anti-viral; spermicidal; anti-tumour; anti-parasitic.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT /note= "N-terminal amino group is mono- or di-substd. by  
FT lipophilic moiety, esp. octanoyl"  
XX  
PN WO9519370-A1.  
XX  
PD 20-JUL-1995.  
XX  
PF 18-JAN-1995; 95WO-US000714.  
XX  
PR 18-JAN-1994; 94US-00184462.  
XX  
PA (MAGA-) MAGAININ PHARM INC.  
XX  
PI Kari U, Williams TJ, McLane M;  
XX  
DR WPI; 1995-263826/34.  
XX  
PT Ion channel-forming amphiphilic peptide(s) with N-terminal lipophilic  
PT gps. - useful e.g. as antiviral, antibacterial, antiparasitic or  
PT antitumour agents.  
XX  
PS Claim 25; Page 108; 139pp; English.  
XX  
CC The present peptide is a specific example corresp. to a highly generic

CC formula for ion channel forming peptides (ionophores). These ionophores  
CC are known to have a broad range of potent antibiotic activity against  
CC microorganisms including gram-positive and gram-negative bacteria, fungi,  
CC viruses, protozoa and parasites. N-terminal modification (pref. mono-  
CC substn. by octanoyl) to produce an ion-channel forming peptide having a  
CC lipophilic N-terminus increases the biological activity of the peptides  
CC against target cells, viruses and virally-infected cells, compared to  
CC peptides substn. with an acetyl group at the N-terminus. Compositions  
CC comprising the peptides with lipophilic modifications are claimed for  
CC inhibiting growth of a target cell, virus or virally-infected cell

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
|||  
Db 1 AKK 3

RESULT 58

AAR91788

ID AAR91788 standard; peptide; 11 AA.

XX

AC AAR91788;

XX

DT 11-JUL-1996 (first entry)

XX

DE Ion-channel forming peptide #123 with lipophilic N-terminal group.

XX

KW Ion channel forming peptide; lipophilic; N-terminal modification;  
KW magainin; inhibition; cell growth; viral replication; ionophore;  
KW membrane permeability; antimicrobial; anti-bacterial; antibiotic;  
KW anti-fungal; anti-viral; sppermicidal; anti-tumour; anti-parasitic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers  
FT Modified-site 1  
FT /note= "N-terminal amino group is mono-substd. by  
FT octanoyl"  
FT Modified-site 11  
FT /note= "C-terminal amide"

XX

PN WO9519370-A1.

XX

PD 20-JUL-1995.

XX

PF 18-JAN-1995; 95WO-US000714.

XX

PR 18-JAN-1994; 94US-00184462.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Kari U, Williams TJ, McLane M;

XX  
DR WPI; 1995-263826/34.  
XX  
PT Ion channel-forming amphiphilic peptide(s) with N-terminal lipophilic  
PT gps. - useful e.g. as antiviral, antibacterial, antiparasitic or  
PT antitumour agents.  
XX  
PS Example 1; Page 111; 139pp; English.  
XX  
CC Various ion channel forming peptides (ionophores) in C-terminal amide  
CC form were modified by N-terminal substn. with a lipophilic group and then  
CC tested for activity against S.aureus ATCC 25923 (S), P.aeruginosa ATCC  
CC 27853 (P), E.coli ATCC 25922 (E) and C.albicans (C). Results indicated  
CC that when a biologically active peptide is substn. with a lipophilic  
CC moiety, the peptide has increased activity against a range of  
CC microorganisms. Compositions comprising such peptides with lipophilic  
CC modifications are claimed for inhibiting growth of a target cell, virus  
CC or virally-infected cell. Minimum inhibitory concentrations (in  
CC microgram/ml) for the present peptide against S, P, E and C,  
CC respectively, were: 32, 16, 32 and 32

XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
      |||  
Db 7 AKK 9

RESULT 59  
AAR91787  
ID AAR91787 standard; peptide; 11 AA.  
XX  
AC AAR91787;  
XX  
DT 11-JUL-1996 (first entry)  
XX  
DE Ion-channel forming peptide #122 with lipophilic N-terminal group.  
XX  
KW Ion channel forming peptide; lipophilic; N-terminal modification;  
KW magainin; inhibition; cell growth; viral replication; ionophore;  
KW membrane permeability; antimicrobial; anti-bacterial; antibiotic;  
KW anti-fungal; anti-viral; spermicidal; anti-tumour; anti-parasitic.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT /note= "N-terminal amino group is mono-substd. by  
FT octanoyl"  
FT Modified-site 11  
FT /note= "C-terminal amide"  
XX  
PN WO9519370-A1.

XX  
PD 20-JUL-1995.  
XX  
PF 18-JAN-1995; 95WO-US000714.  
XX  
PR 18-JAN-1994; 94US-00184462.  
XX  
PA (MAGA-) MAGAININ PHARM INC.  
XX  
PI Kari U, Williams TJ, McLane M;  
XX  
DR WPI; 1995-263826/34.  
XX  
PT Ion channel-forming amphiphilic peptide(s) with N-terminal lipophilic  
PT gps. - useful e.g. as antiviral, antibacterial, antiparasitic or  
PT antitumour agents.  
XX  
PS Example 1; Page 111; 139pp; English.  
XX  
CC Various ion channel forming peptides (ionophores) in C-terminal amide  
CC form were modified by N-terminal substn. with a lipophilic group and then  
CC tested for activity against S.aureus ATCC 25923 (S), P.aeruginosa ATCC  
CC 27853 (P), E.coli ATCC 25922 (E) and C.albicans (C). Results indicated  
CC that when a biologically active peptide is substd. with a lipophilic  
CC moiety, the peptide has increased activity against a range of  
CC microorganisms. Compositions comprising such peptides with lipophilic  
CC modifications are claimed for inhibiting growth of a target cell, virus  
CC or virally-infected cell. Minimum inhibitory concentrations (in  
CC microgram/ml) for the present peptide against S, P, E and C,  
CC respectively, were: 32, 32, 64 and 64  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 7 AKK 9

RESULT 60  
AAR87902  
ID AAR87902 standard; peptide; 11 AA.  
XX  
AC AAR87902;  
XX  
DT 28-FEB-1996 (first entry)  
XX  
DE Neuropeptide Y agonist peptide.  
XX  
KW neuropeptide Y; NPY; agonist; hypertensive; vasoconstrictor;  
KW colon relaxing; gastric emptying diminution; eating disorder;  
KW anorexia nervosa.  
XX  
OS Synthetic.

XX  
FH Key Location/Qualifiers  
FT Modified-site 2  
FT /label= OTHER  
FT /note= "8-amino-octanoic acid residue"  
FT Modified-site 11  
FT /note= "Tyr-NH2"  
XX  
PN US5395823-A.  
XX  
PD 07-MAR-1995.  
XX  
PF 15-MAR-1993; 93US-00032526.  
XX  
PR 26-AUG-1988; 88US-00237591.  
PR 24-JUL-1989; 89US-00384373.  
PR 21-DEC-1990; 90US-00631755.  
PR 18-OCT-1991; 91US-00782890.  
PR 05-AUG-1992; 92US-00925546.  
XX  
PA (RICH ) MERRELL DOW PHARM INC.  
XX  
PI Krstenansky JL;  
XX  
DR WPI; 1995-114851/15.  
XX  
PT New peptide agonists of neuropeptide Y - useful for increasing blood  
PT pressure and treating eating disorders such as anorexia nervosa.  
XX  
PS Example 9; Col 9; 7pp; English.  
XX  
CC The patent relates to a new group of peptides which have neuropeptide Y  
CC agonist action. The peptides have hypertensive activity, vasoconstricting  
CC activity, colon relaxing activity and gastric emptying diminution  
CC activity. They are of particular use in treatment of eating disorders  
CC such as anorexia nervosa. The present sequence is that of a peptide  
CC prepared in the Examples of the patent, but it does not appear to fit the  
CC generic formulae of the active compounds  
XX  
SQ Sequence 11 AA;  
  
Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 RQR 7  
|||  
Db 8 RQR 10  
  
RESULT 61  
AAW49555  
ID AAW49555 standard; peptide; 11 AA.  
XX  
AC AAW49555;  
XX  
DT 05-JUN-1998 (first entry)

XX  
DE Human leucocyte antigen DQ4 binding peptide #446.  
XX  
KW Human leucocyte antigen; HLA-DQ4; combinatorial library;  
KW autoimmune disease; chronic articular rheumatism.  
XX  
OS Synthetic.  
XX  
PN JP08151396-A.  
XX  
PD 11-JUN-1996.  
XX  
PF 28-NOV-1994; 94JP-00292657.  
XX  
PR 28-NOV-1994; 94JP-00292657.  
XX  
PA (TEIJ ) TEIJIN LTD.  
XX  
DR WPI; 1996-329479/33.  
XX  
PT HLA-binding oligopeptide and an immuno:regulator contg it - used in the  
PT treatment of auto:immune disease.  
XX  
PS Claim 4; Page 49; 61pp; Japanese.  
XX  
CC This peptide is an example of a peptide which binds to a human leucocyte  
CC antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid  
CC combinatorial library comprising the sequence AAV05953, by screening with  
CC an HLA-DQ4 molecule. The peptide is used for the treatment of autoimmune  
CC disease, or especially for treatment of viral diseases  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 6 RQR 8

RESULT 62  
AAR96835  
ID AAR96835 standard; peptide; 11 AA.  
XX  
AC AAR96835;  
XX  
DT 29-NOV-1996 (first entry)  
XX  
DE Human neurofilament triplet h fragment, homologous to *Neisseria* IgA-  
DE alpha1.  
XX  
KW IgA protease precursor; IPP; bacterial polyprotein; autoimmune;  
KW viral infection; rheumatoid arthritis; AIDS; meningococcal bacteria;  
KW human neurofilament triplet h protein; Nfh; *Neisseria* gonorrhoeae; MS11.  
XX

OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 1. .3  
FT /note= "identical to sequence in Neisseria gonorrhoeae  
FT Iga-alpha1"  
FT Region 5. .7  
FT /note= "identical to sequence in Neisseria gonorrhoeae  
FT Iga-alpha1"  
FT Region 10. .11  
FT /note= "identical to sequence in Neisseria gonorrhoeae  
FT Iga-alpha1"  
XX  
PN WO9609395-A2.  
XX  
PD 28-MAR-1996.  
XX  
PF 21-SEP-1995; 95WO-EP003726.  
XX  
PR 21-SEP-1994; 94DE-04433708.  
XX  
PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
XX  
PI Meyer TF, Pohlner J, Beck SC, Jose J, Woelk U, Lorenzen DR;  
PI Oetzelberger KB;  
XX  
DR WPI; 1996-188456/19.  
XX  
PT Medicaments for treating auto-immune or viral diseases - contg.  
PT substances interfering with bacterial poly:protein function.  
XX  
PS Claim 32; Fig 2; 117pp; German.  
XX  
CC The present sequence from human neurofilament triplet h protein has  
CC homology to a cleavage product from the Iga-alpha1 domain of the  
CC precursor of IgA-protease polyprotein (IPP) of Neisseria gonorrhoeae  
CC strain MS11. The Neisseria IPP has been implicated in rheumatoid  
CC arthritis and other auto-immune diseases. The polyprotein also activates  
CC proviruses, including HIV. Substances which interfere with the function  
CC of IPP from Neisseria will be useful for treating associated autoimmune  
CC diseases and viral infections. Peptides comprising the homology region  
CC sequences, whether from Neisseria or from humans, are claimed  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 2 RQR 4

RESULT 63  
AAR85318  
ID AAR85318 standard; peptide; 11 AA.

XX  
AC AAR85318;  
XX  
DT 25-MAR-2003 (revised)  
DT 19-AUG-1996 (first entry)  
XX  
DE Human retinoic acid receptor RAR-beta (human liver HAP) peptide-2.  
XX  
KW HAP; liver; hepatoma; retinoic acid receptor; RAR-beta; psoriasis;  
KW atherosclerosis; rheumatoid arthritis.  
XX  
OS Homo sapiens.  
XX  
PN US5468617-A.  
XX  
PD 21-NOV-1995.  
XX  
PF 02-FEB-1994; 94US-00190555.  
XX  
PR 16-DEC-1987; 87US-00133687.  
PR 17-DEC-1987; 87US-00134130.  
PR 20-JUN-1988; 88US-00209009.  
PR 30-NOV-1988; 88US-00278136.  
PR 30-MAR-1989; 89US-00330405.  
PR 21-AUG-1991; 91US-00751612.  
PR 30-MAR-1992; 92US-00860577.  
PR 11-DEC-1992; 92US-00989902.  
PR 22-JUL-1993; 93US-00095706.  
XX  
PA (TIOL/) TIOLLAIS P.  
PA (DEJE/) DEJEAN A.  
PA (KRUS/) KRUST A.  
PA (PETK/) PETKOVICH M.  
PA (DTHE/) BLAUDIN DE THE H.  
PA (MARC/) MARCHIO A.  
PA (BRAN/) BRAND N.  
PA (CHAM/) CHAMBON P.  
XX  
PI Brand N, Chambon P, Blaudin De The H, Marchio A, Dejean A;  
PI Petkovich M, Krust A, Tiollais P;  
XX  
DR WPI; 1996-010094/01.  
XX  
PT Method for screening for retinoic acid receptor-beta (ant)agonists -  
PT useful for blood testing and for treatment of rheumatoid arthritis,  
PT psoriasis, atherosclerosis etc.  
XX  
PS Claim 7; Col 39-40; 35pp; English.  
XX  
CC This RAR-beta peptide-2 fragment is part of a protein which may be  
CC expressed recombinantly in bacterial host cells such as Escherichia coli  
CC TG-1. The protein, which is free from human, blood-derived protein, forms  
CC a complex with an agonist or antagonist. The protein may be used in a  
CC novel method for assaying a fluid for the presence of an agonist or  
CC antagonist to retinoic acid receptor, RAR-beta. (Updated on 25-MAR-2003  
CC to correct PF field.)  
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 4  
|||  
Db 7 KKE 9

RESULT 64

AAW18499

ID AAW18499 standard; peptide; 11 AA.

XX

AC AAW18499;

XX

DT 19-FEB-1998 (first entry)

XX

DE Amino-terminal peptide 1 associated with novel helicase.

XX

KW Nucleic acid binding protein; helicase; leflunomide; assaying;  
KW 4-(N-(4-trifluoromethylphenyl)-5-methyl-isoxazole; identification;  
KW anticancer; antiatherosclerotic; immunosuppressant; sequencing;  
KW antiinflammatory; antiviral; antifungal; antibacterial; treatment;  
KW Alzheimer's disease; cancer; rheumatism; arthrosis; determination;  
KW atherosclerosis; osteoporosis; acute infection; chronic infection;  
KW autoimmune disease; diabetes; organ transplant; isolation;  
KW amino-terminal.

XX

OS Homo sapiens.

XX

PN DE19545126-A1.

XX

PD 05-JUN-1997.

XX

PF 04-DEC-1995; 95DE-01045126.

XX

PR 04-DEC-1995; 95DE-01045126.

XX

PA (FARH ) HOECHST AG.

XX

PI Kirschbaum B, Muellner S, Bartlett R;

XX

DR WPI; 1997-299388/28.

XX

PT New nucleic acid binding protein with helicase activity - is strongly  
PT induced by leflunomide, used to isolate specific binding RNA and for  
PT identifying substances with anticancer, antiviral etc. activities.

XX

PS Example 4; Page 15; 28pp; German.

XX

CC The present sequence is an amino-terminal peptide associated with a novel  
CC nucleic acid binding protein with helicase activity, the mRNA of which  
CC (or its translation products) is strongly expressed in presence of  
CC leflunomide, i.e. 4-(N-(4-trifluoromethylphenyl)-5-methyl-isoxazole, or a  
CC compound with similar activity. The helicase can be used in assay systems

CC to identify/discover anticancer, antiatherosclerotic, immunosuppressing,  
CC antiinflammatory, antiviral, antifungal and antibacterial agents, e.g. to  
CC treat Alzheimer's disease, cancer, rheumatism, arthrosis,  
CC atherosclerosis, osteoporosis, acute/chronic infections, autoimmune  
CC disease, diabetes and complications of organ transplants, and to isolate  
CC or determine the sequences of specific binding RNA  
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4  
|||  
Db 9 KKE 11

RESULT 65

AAW24438

ID AAW24438 standard; peptide; 11 AA.

XX

AC AAW24438;

XX

DT 30-SEP-1997 (first entry)

XX

DE Nucleic acid (NA) binding peptide used in NA delivery to cells.

XX

KW Nucleic acid transporter; gene therapy; binding complex; lysis agent;

KW JTS-1; K8; alpha helix; endosome; lysosome; nucleus targeting.

XX

OS Synthetic.

XX

PN WO9640958-A1.

XX

PD 19-DEC-1996.

XX

PF 23-APR-1996; 96WO-US005679.

XX

PR 07-JUN-1995; 95US-00484777.

XX

PA (BAYU ) BAYLOR COLLEGE MEDICINE.

XX

PI Smith LC, Sparrow JT, Woo SL;

XX

DR WPI; 1997-052345/05.

XX

PT Nucleic acid transporter useful in gene therapy - contains binding  
PT complex associated with surface and nuclear ligands and lysis agent.

XX

PS Disclosure; Page 49; 125pp; English.

XX

CC AAW24434-W24459 are nucleic acid (NA) binding peptides, capable of both  
CC condensing and stabilising a NA. The peptides can be conjugated to a  
CC lytic peptide to form a nucleic acid transporter system. The lysis agent  
CC forms an alpha-helical structure. The transporter system is used to  
CC deliver nucleic acid to a cell and for treating humans by gene therapy.

CC By taking advantage of the characteristics of both the lysis agents and  
CC the binding molecules, delivery of the nucleic acid is enhanced. Specific  
CC lysis agents are capable of releasing the nucleic acid into the cellular  
CC interior from the endosome. Release is efficient without  
CC endosomal/lysosomal degradation. Once released the binding complexes help  
CC target the nucleic acid to the nucleus  
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
|||  
Db 3 AKK 5

RESULT 66

AAW34642

ID AAW34642 standard; peptide; 11 AA.

XX

AC AAW34642;

XX

DT 02-MAR-1998 (first entry)

XX

DE Control peptide.

XX

KW Occludin; inhibitor; human; drug absorption; drug delivery; gene therapy;  
KW tissue permeability; cell adhesion; antibody.

XX

OS Synthetic.

XX

PN WO9733605-A1.

XX

PD 18-SEP-1997.

XX

PF 14-MAR-1997; 97WO-US005809.

XX

PR 15-MAR-1996; 96US-0013625P.

XX

PA (UYYA ) UNIV YALE.

XX

PI Anderson JM, Van Itallie CM;

XX

DR WPI; 1997-470640/43.

XX

PT Isolated human occludin protein - useful for increasing drug delivery  
PT across endothelial or epithelial barriers, or for reducing tissue  
PT permeability.

XX

PS Disclosure; Page 36; 49pp; English.

XX

CC This control peptide was used in experiments to demonstrate inhibition of  
CC occludin-dependent intercellular adhesion using extracellular loop  
CC peptides corresponding to the N-terminal half of occludin extracellular  
CC loop 1 (see AAW34639) and the C-terminal half of extracellular loop 1

CC (see AAW34640. Inhibitors of human occludin inhibitors can be used to  
CC enhance delivery of drugs (or gene therapy vectors) by increasing  
CC absorption across endothelial or epithelial barriers, i.e. transmucosal  
CC or transvascular drug delivery. Inhibitors include occludin surface loop  
CC peptides that inhibit adhesion and/or barrier properties, or antibodies  
CC that interact with occludin or occludin receptors  
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RKD 9  
|||  
Db 7 RKD 9

RESULT 67

AAW09909

ID AAW09909 standard; peptide; 11 AA.

XX

AC AAW09909;

XX

DT 16-OCT-1997 (first entry)

XX

DE Prostate specific membrane antigen peptide PSM-P26.

XX

KW Prostate specific membrane antigen; PSMA; prostate specific antigen; PSA;  
KW prostate cancer; adoptive cellular immunotherapy; therapy; vaccine.

XX

OS Homo sapiens.

XX

PN WO9704802-A1.

XX

PD 13-FEB-1997.

XX

PF 29-JUL-1996; 96WO-US012389.

XX

PR 31-JUL-1995; 95US-00509254.

XX

PA (PACI-) PACIFIC NORTHWEST CANCER FOUND.

XX

PI Murphy GP, Boynton AL, Tjoa BA;

XX

DR WPI; 1997-145375/13.

XX

PT Use of dendritic cells for prostate cancer immuno:therapy - the cells are  
PT exposed to prostate cancer antigen, then administered to the patient  
PT where they activate and proliferate T-cells.

XX

PS Claim 3; Page 47; 69pp; English.

XX

CC Peptide PSM-P26 (AAW09909) corresponds to amino acid residues 398-408 of  
CC prostate specific membrane antigen (PSMA). A method for producing a  
CC cancer growth inhibiting response comprises exposing human dendritic  
CC cells (DCs) to PSM-P26 or other PSMA or prostate specific antigen

CC peptides (see also AAW09889-908 and AAW09910-26), and then administering  
CC the DCs to a prostate cancer patient to activate T cell responses in  
CC vivo. Alternatively, the T cell response is activated in vitro and the T  
CC cells are then administered to the patient. In either case, the DCs are  
CC used to elicit an immunotherapeutic growth inhibiting response against a  
CC primary or metastatic prostate tumour. PSM-P26 was selected to be  
CC presented by DCs to activate T cells of a patient which match the A11  
CC haplotype

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4  
|||  
Db 9 KKE 11

RESULT 68

AAW10140

ID AAW10140 standard; peptide; 11 AA.

XX

AC AAW10140;

XX

DT 25-MAR-2003 (revised)

DT 02-OCT-1997 (first entry)

XX

DE Hepatitis C virus peptide antigen IIA.

XX

KW Antibody; HCV; immunoassay; vaccine; mimic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1  
FT /note= "H or a linker arm by which the peptide can be  
FT attached to a carrier or solid phase comprising at least  
FT one amino acid and as many as 60, most frequently 1-20  
FT amino acids, such as Cys, Lys, Tyr, Glu or Asp, or  
FT chemical groups such as biotin or thioglycolic acid; can  
FT be modified by acetylation"

FT Modified-site 11  
FT /note= "A bond or a linker arm by which the peptide can  
FT be attached to a carrier or solid phase comprising at  
FT least one amino acid and as many as 60 amino acids, most  
FT frequently 1-10 amino acids, such as Cys, Lys, Tyr, Asp,  
FT or chemical groups such as biotin or thioglycolic acid;  
FT and attached on to that is NH2, OH or a linkage involving  
FT either of these two groups"

XX

PN EP754704-A2.

XX

PD 22-JAN-1997.

XX

PF 14-DEC-1990; 96EP-00201157.

XX  
PR 14-DEC-1990; 90EP-00124241.  
XX  
PA (INNO-) INNOGENETICS NV.  
XX  
PI Deleys RJ, Pollet D, Maertens G, Van Heuverswyn H;  
XX  
DR WPI; 1997-089256/09.  
XX  
PT Hepatitis C virus peptide mimics - for use in immunoassays, vaccines,  
PT etc.  
XX  
PS Claim 2; Page 38; 65pp; English.  
XX  
CC The present sequence represents a novel synthetic Hepatitis C virus (HCV)  
CC antigen IIA for the detection of antibodies. The peptide contains  
CC modifications at the N- and C-terminal (see features table) with the  
CC condition that if the modification represents an amino acid(s), that they  
CC are different from any naturally occurring HCV flanking regions. The  
CC peptide represents an HCV peptide mimic and may be used as an immunoassay  
CC reagent for detecting antibodies to HCV; for incorporation into vaccines  
CC against HCV; and for raising antibodies against HCV. (Updated on 25-MAR-  
CC 2003 to correct PF field.)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QRK 8  
|||  
Db 1 QRK 3

RESULT 69  
AAW62116  
ID AAW62116 standard; peptide; 11 AA.  
XX  
AC AAW62116;  
XX  
DT 16-SEP-1998 (first entry)  
XX  
DE Human MDM2 binding peptide 5.  
XX  
KW Identification; ligand; biological activity; target-binding;  
KW drug screening; library; inhibitory ligand.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9819162-A1.  
XX  
PD 07-MAY-1998.  
XX  
PF 31-OCT-1997; 97WO-US019638.  
XX

PR 31-OCT-1996; 96US-00740671.

XX

PA (NOVA-) NOVALON PHARM CORP.

XX

PI Fowlkes DM, Kay BK, Frelinger JA, Hyde-Deruyscher RP;

XX

DR WPI; 1998-272389/24.

XX

PT Identifying ligands which mediate biological activity of a protein - by identifying target-binding ligands and screening a library for ligands which inhibit target-binding ligand mediated activity.

XX

PS Example 3; Page 93; 143pp; English.

XX

CC A method has been developed for identifying a ligand which mediates the biological activity of a target protein (T) by inhibiting the binding of (T) to a binding partner. The method comprises: (a) screening a first combinatorial library comprising first member ligands for binding to the target-binding ligands (TBLs), to identifying one or more TBLs; (b) screening a second library comprising second member ligands for the ability to inhibit the binding of one or more of the TBLs to the target protein, and so obtaining one or more inhibitory ligands; and (c) determining which of the inhibitory ligands can mediate a biological activity of the target protein. The present sequence represents a potential binding peptide for human MDM2 from an example of the present invention. The method can be used for identifying drugs which can mediate the biological activity of a target protein. It can be used to identify the biological activity of a target protein whose biological function is not known and perhaps cannot be determined directly. The method can also be used to identify new inhibitory ligands of specific target proteins. The method provides high throughput screens which are essentially identical for similar and dissimilar targets, bypassing the need to develop distinct assays for biochemically diverse targets

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4

|||

Db 8 KKE 10

RESULT 70

AAW66523

ID AAW66523 standard; peptide; 11 AA.

XX

AC AAW66523;

XX

DT 25-NOV-1998 (first entry)

XX

DE Amphiphilic peptide.

XX

KW magainin; analogue; antimicrobial; antitumour; wound healing; CPF;  
KW amphiphilic; XPF peptide.

XX  
OS Synthetic.  
XX  
PN US5792831-A.  
XX  
PD 11-AUG-1998.  
XX  
PF 17-NOV-1994; 94US-00343882.  
XX  
PR 08-FEB-1990; 90US-00476629.  
PR 14-MAY-1990; 90US-00522688.  
PR 28-APR-1992; 92US-00874685.  
PR 05-OCT-1993; 93US-00133740.  
XX  
PA (MAGA-) MAGAININ PHARM INC.  
XX  
PI Maloy WL;  
XX  
DR WPI; 1998-456190/39.  
XX  
PT Magainin peptide analogues - useful as antimicrobial or antitumour  
PT agents, etc.  
XX  
PS Disclosure; Col 20; 25pp; English.  
XX  
CC The invention relates to analogues of a magainin I or II, D-form  
CC analogues, deletion analogues or related peptides. It also relates to  
CC basic polypeptides having at least 16 amino acids, including at least 8  
CC hydrophobic amino acids and at least 8 hydrophilic amino acids. The  
CC peptides may be used as antimicrobial agents, antiviral agents,  
CC antibiotics, antitumour agents, antiparasitic agents, spermicides,  
CC preservatives or sterilants, or agents for promoting wound healing. The  
CC present sequence represents a specific example of a peptide disclosed in  
CC the specification  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 1 AKK 3

RESULT 71  
AAW80589  
ID AAW80589 standard; peptide; 11 AA.  
XX  
AC AAW80589;  
XX  
DT 18-DEC-1998 (first entry)  
XX  
DE src-family tyrosine kinase peptide fragment.  
XX  
KW src-family tyrosine kinase; serine phosphorylation-mediated degradation;

KW mutation; T cell activation; immune response; screening; cancerous cell; KW therapy; immunity; allogenic transplant; xenogeneic organ transplant.

XX

OS Mus sp.

XX

FH Key Location/Qualifiers

FT Misc-difference 8

FT /note= "can be replaced with Ala"

FT Misc-difference 9

FT /note= "can be replaced with Ala"

XX

PN WO9846996-A2.

XX

PD 22-OCT-1998.

XX

PF 10-APR-1998; 98WO-IB000801.

XX

PR 11-APR-1997; 97US-0041878P.

XX

PA (ROBA-) ROBARTS RES INST JOHN P.

XX

PI Madrenas J;

XX

DR WPI; 1998-583294/49.

XX

PT Detection of levels of T cell activation - by measuring increase in PT amount of serine phosphorylated Ick relative to total Ick as indicative PT of increased T cell activation.

XX

PS Claim 23; Page 27; 48pp; English.

XX

CC This represents a peptide fragment of the src-family tyrosine kinase CC polypeptide. The invention provides src-family tyrosine kinase peptide CC fragments (AAW80586 to AAW80591), which on mutation reduces the serine CC phosphorylation-mediated degradation of the polypeptide. The mutation CC could be a mutation of the serine residue located at the amino terminus CC to alanine and/or could be a mutation that results in a leucine- leucine CC to alanine-alanine change in the polypeptide. The invention also provides CC methods for detecting the level of T cell activation; for detecting a CC compound that modulates T cell activation; and for generating a src- CC family tyrosine kinase polypeptide that has a reduced level of serine CC phosphorylation-mediated degradation. The methods can be used for the CC rapid detection of an antigen-specific immune response. They can also be CC used for screening candidate therapeutic compounds and protocols for the CC efficacy in either stimulating or blocking the antigen-specific immune CC response. Identification and development of such compounds and protocols CC is useful for enhancing, decreasing or preventing antigen- specific CC immune responses. Therapies which enhance the immune response aid in the CC development of immunity to antigens derived from pathogens and cancerous CC cells. Therapies which prevent or decrease the development of an antigen- CC specific immune response are useful in preventing an immune response to CC antigens derived from e.g. allogenic or xenogeneic organ transplants

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.8e+03;

Matches	3;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	7	RKD 9							
Db	1	RKD 3							

RESULT 72

AAW64653

ID AAW64653 standard; peptide; 11 AA.

XX

AC AAW64653;

XX

DT 23-OCT-1998 (first entry)

XX

DE Synthetic SEB-related peptide (position 51-61).

XX

KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;  
KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;  
KW therapeutic; vaccine; food poisoning.

XX

OS Synthetic.

OS Staphylococcus aureus.

XX

PN WO9829444-A1.

XX

PD 09-JUL-1998.

XX

PF 30-DEC-1997; 97WO-IL000438.

XX

PR 30-DEC-1996; 96IL-00119938.

XX

PA (YISS ) YISSUM RES & DEV CO.

XX

PI Kaempfer R, Arad G;

XX

DR WPI; 1998-388042/33.

XX

PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.

PT antagonising toxin-mediated activation of T cells and prevention or

PT treatment of toxic shock caused by exotoxin(s).

XX

PS Example 2; Page 38; 68pp; English.

XX

CC AAW64636-W64657 are peptides homologous to the amino acid sequence of a  
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide  
CC capable of eliciting protective immunity against toxic shock induced by  
CC PET or by a mixture of PETs. Such peptides are also capable of  
CC antagonising toxin-mediated activation of T-cells, inhibiting expression  
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or TNF-  
CC beta genes. The peptides may be used to prepare therapeutics or vaccines  
CC for the treatment of prophylaxis of toxin-mediated activation of T cells  
CC and eliciting protective immunity against toxic shock induced by PETs.  
CC They can also be used for the treatment of harmful effects (especially  
CC food poisoning) and toxic shock caused by PET. Antiserum to the peptides  
CC can also be used for alleviating toxic shock induced by PET

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10  
|||  
Db 4 KDT 6

RESULT 73

AAW51825

ID AAW51825 standard; peptide; 11 AA.

XX

AC AAW51825;

XX

DT 13-OCT-1998 (first entry)

XX

DE Peptide YY analogue #26.

XX

KW peptide YY; cell proliferation; nutrient transport; lipolysis;

KW electrolyte secretion; anti-secretory; intestinal water; antimotility.

XX

OS Synthetic.

OS Mammalia.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal acetyl"

FT Modified-site 11

FT /note= "C-terminal amide"

XX

PN WO9820885-A1.

XX

PD 22-MAY-1998.

XX

PF 13-NOV-1996; 96WO-US018374.

XX

PR 13-NOV-1996; 96WO-US018374.

XX

PA (UYCI-) UNIV CINCINNATI.

XX

PI Balasubramaniam A;

XX

DR WPI; 1998-322327/28.

XX

PT New analogue(s) of peptide YY - used, e.g. to control cell proliferation,

PT nutrient transport, lipolysis and intestinal water and electrolyte

PT secretion.

XX

PS Disclosure; Page 17; 54pp; English.

XX

CC The invention relates to peptide YY analogues which may be used e.g. for  
CC decreasing excess intestinal water and electrolyte secretion in mammals,  
CC to regulate cell proliferation (especially intestinal cell  
CC proliferation), to increase nutrient transport, to regulate lipolysis and

CC to regulate blood flow. The peptides exhibit antisecretory and  
CC antimotility properties and are especially useful in treatment of  
CC gastrointestinal disorders associated with excess intestinal electrolyte  
CC and water secretion as well as decreased absorption. The new peptides are  
CC truncated versions of peptide YY. They interact solely with peptide YY  
CC receptors and not with homologous receptors such as NPY Y1 and Y3, thus  
CC minimising unwanted (ant)agonist side reactions. The present sequence  
CC represents a peptide YY analogue  
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 8 RQR 10

RESULT 74

AAW84029

ID AAW84029 standard; peptide; 11 AA.

XX

AC AAW84029;

XX

DT 05-FEB-1999 (first entry)

XX

DE Human CYP3A4 specific synthetic peptide fragment 18.

XX

KW CYP3A4; epitope; anti-peptide antibody; enzyme; therapeutic agent;  
KW cytochrome P450; gene expression; tissue localisation; inhibitory;  
KW affinity purification; human.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9844939-A1.

XX

PD 15-OCT-1998.

XX

PF 09-APR-1998; 98WO-US007165.

XX

PR 10-APR-1997; 97US-0043230P.

XX

PA (MERI ) MERCK & CO INC.

XX

PI Lu AYH, Wang RW;

XX

DR WPI; 1998-609899/51.

XX

PT New antibodies to human CYP3A4 - are specific relative to other human  
PT P450 enzymes, produced using peptides specific for human CYP3A4.

XX

PS Example 2; Page 24; 58pp; English.

XX

CC Sequences AAW84012 to AAW84039 represent synthetic peptides specific to

CC human CYP3A4. The peptides are fragments contained within the peptide  
CC AAW84012 or AAW84013 comprising an inhibitory epitope. The invention  
CC provides anti-peptide antibodies raised against such human CYP3A4  
CC specific peptides in relation to other human P450 enzymes and inhibit  
CC human CYP3A4 activity. The inhibitory anti-peptide antibodies are used  
CC for evaluating the role of human CYP3A4 in mediating in vitro metabolism  
CC of therapeutic agents. In addition, the antibodies can be used for  
CC cytochrome P450 epitope investigation, gene expression and regulation,  
CC tissue localisation, affinity purification for CYP3A4 and many other  
CC studies

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DTQ 11  
|||  
Db 1 DTQ 3

RESULT 75

AAW84023

ID AAW84023 standard; peptide; 11 AA.

XX

AC AAW84023;

XX

DT 05-FEB-1999 (first entry)

XX

DE Human CYP3A4 specific synthetic peptide fragment 12.

XX

KW CYP3A4; epitope; anti-peptide antibody; enzyme; therapeutic agent;  
KW cytochrome P450; gene expression; tissue localisation; inhibitory;  
KW affinity purification; human.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9844939-A1.

XX

PD 15-OCT-1998.

XX

PF 09-APR-1998; 98WO-US007165.

XX

PR 10-APR-1997; 97US-0043230P.

XX

PA (MERI ) MERCK & CO INC.

XX

PI Lu AYH, Wang RW;

XX

DR WPI; 1998-609899/51.

XX

PT New antibodies to human CYP3A4 - are specific relative to other human  
PT P450 enzymes, produced using peptides specific for human CYP3A4.

XX

PS Example 2; Page 24; 58pp; English.

XX

CC Sequences AAW84012 to AAW84039 represent synthetic peptides specific to  
CC human CYP3A4. The peptides are fragments contained within the peptide  
CC AAW84012 or AAW84013 comprising an inhibitory epitope. The invention  
CC provides anti-peptide antibodies raised against such human CYP3A4  
CC specific peptides in relation to other human P450 enzymes and inhibit  
CC human CYP3A4 activity. The inhibitory anti-peptide antibodies are used  
CC for evaluating the role of human CYP3A4 in mediating in vitro metabolism  
CC of therapeutic agents. In addition, the antibodies can be used for  
CC cytochrome P450 epitope investigation, gene expression and regulation,  
CC tissue localisation, affinity purification for CYP3A4 and many other  
CC studies

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DTQ 11  
|||  
Db 7 DTQ 9

Search completed: April 8, 2004, 15:39:49  
Job time : 46.3077 secs

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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:08 ; Search time 11.3077 Seconds  
(without alignments)  
50.221 Million cell updates/sec

Title: US-09-787-443A-2

Perfect score: 11

Sequence: 1 AKKERQRKDTQ 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8542

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

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6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	4	36.4	11	1	US-08-185-448-5	Sequence 5, Appli
2	4	36.4	11	1	US-08-476-405A-10	Sequence 10, Appl
3	4	36.4	11	1	US-08-476-405A-11	Sequence 11, Appl
4	4	36.4	11	2	US-08-747-137-63	Sequence 63, Appl
5	4	36.4	11	3	US-09-100-930A-10	Sequence 10, Appl
6	3	27.3	11	1	US-08-193-521-18	Sequence 18, Appl
7	3	27.3	11	1	US-08-197-793-8	Sequence 8, Appli
8	3	27.3	11	1	US-08-116-733-32	Sequence 32, Appl
9	3	27.3	11	1	US-08-329-151-26	Sequence 26, Appl
10	3	27.3	11	1	US-08-306-546C-25	Sequence 25, Appl
11	3	27.3	11	1	US-08-434-120-112	Sequence 112, App

12	3	27.3	11	1	US-08-486-057B-16	Sequence 16, Appl
13	3	27.3	11	1	US-08-465-325-111	Sequence 111, App
14	3	27.3	11	1	US-08-465-325-122	Sequence 122, App
15	3	27.3	11	1	US-08-465-325-123	Sequence 123, App
16	3	27.3	11	1	US-08-411-727-10	Sequence 10, Appl
17	3	27.3	11	1	US-08-411-727-18	Sequence 18, Appl
18	3	27.3	11	1	US-08-548-540-119	Sequence 119, App
19	3	27.3	11	2	US-08-530-524A-25	Sequence 25, Appl
20	3	27.3	11	2	US-08-248-839C-26	Sequence 26, Appl
21	3	27.3	11	2	US-08-636-176-8	Sequence 8, Appli
22	3	27.3	11	2	US-08-737-085A-12	Sequence 12, Appl
23	3	27.3	11	2	US-08-538-960-8	Sequence 8, Appli
24	3	27.3	11	2	US-08-893-853-54	Sequence 54, Appl
25	3	27.3	11	2	US-08-893-853-74	Sequence 74, Appl
26	3	27.3	11	2	US-08-466-975A-3	Sequence 3, Appli
27	3	27.3	11	2	US-08-391-671A-3	Sequence 3, Appli
28	3	27.3	11	2	US-08-789-588-16	Sequence 16, Appl
29	3	27.3	11	2	US-08-760-075A-1	Sequence 1, Appli
30	3	27.3	11	2	US-08-706-741B-54	Sequence 54, Appl
31	3	27.3	11	2	US-08-924-695A-54	Sequence 54, Appl
32	3	27.3	11	3	US-08-467-902A-3	Sequence 3, Appli
33	3	27.3	11	3	US-09-246-258-12	Sequence 12, Appl
34	3	27.3	11	3	US-09-188-579-65	Sequence 65, Appl
35	3	27.3	11	3	US-08-602-999A-284	Sequence 284, App
36	3	27.3	11	3	US-09-113-921-74	Sequence 74, Appl
37	3	27.3	11	3	US-08-659-254-8	Sequence 8, Appli
38	3	27.3	11	3	US-09-206-059-23	Sequence 23, Appl
39	3	27.3	11	3	US-09-208-966-2	Sequence 2, Appli
40	3	27.3	11	3	US-09-208-966-16	Sequence 16, Appl
41	3	27.3	11	3	US-09-208-966-52	Sequence 52, Appl
42	3	27.3	11	3	US-08-647-405B-6	Sequence 6, Appli
43	3	27.3	11	3	US-09-177-249-204	Sequence 204, App
44	3	27.3	11	3	US-09-315-444-65	Sequence 65, Appl
45	3	27.3	11	3	US-09-532-106-12	Sequence 12, Appl
46	3	27.3	11	3	US-09-338-546-1	Sequence 1, Appli
47	3	27.3	11	3	US-09-142-732-6	Sequence 6, Appli
48	3	27.3	11	3	US-09-044-411-1	Sequence 1, Appli
49	3	27.3	11	3	US-09-044-411-2	Sequence 2, Appli
50	3	27.3	11	3	US-09-044-411-3	Sequence 3, Appli
51	3	27.3	11	3	US-09-044-411-4	Sequence 4, Appli
52	3	27.3	11	3	US-09-044-411-5	Sequence 5, Appli
53	3	27.3	11	3	US-09-044-411-6	Sequence 6, Appli
54	3	27.3	11	3	US-09-044-411-8	Sequence 8, Appli
55	3	27.3	11	3	US-09-133-062D-28	Sequence 28, Appl
56	3	27.3	11	3	US-09-133-062D-29	Sequence 29, Appl
57	3	27.3	11	3	US-09-275-265-3	Sequence 3, Appli
58	3	27.3	11	4	US-09-057-897-8	Sequence 8, Appli
59	3	27.3	11	4	US-09-057-897-13	Sequence 13, Appl
60	3	27.3	11	4	US-09-057-897-18	Sequence 18, Appl
61	3	27.3	11	4	US-09-296-089-37	Sequence 37, Appl
62	3	27.3	11	4	US-09-025-596-34	Sequence 34, Appl
63	3	27.3	11	4	US-09-115-737-111	Sequence 111, App
64	3	27.3	11	4	US-09-115-737-122	Sequence 122, App
65	3	27.3	11	4	US-09-115-737-123	Sequence 123, App
66	3	27.3	11	4	US-09-187-859-3110	Sequence 3110, Ap
67	3	27.3	11	4	US-09-187-859-3155	Sequence 3155, Ap
68	3	27.3	11	4	US-09-187-859-3200	Sequence 3200, Ap

69	3	27.3	11	4	US-09-187-859-3245	Sequence 3245, Ap
70	3	27.3	11	4	US-09-187-859-3290	Sequence 3290, Ap
71	3	27.3	11	4	US-09-187-859-3341	Sequence 3341, Ap
72	3	27.3	11	4	US-09-187-859-3383	Sequence 3383, Ap
73	3	27.3	11	4	US-09-187-859-3425	Sequence 3425, Ap
74	3	27.3	11	4	US-09-187-859-3467	Sequence 3467, Ap
75	3	27.3	11	4	US-09-187-859-3509	Sequence 3509, Ap
76	3	27.3	11	4	US-09-446-047A-12	Sequence 12, Appl
77	3	27.3	11	4	US-09-659-084-1	Sequence 1, Appli
78	3	27.3	11	4	US-09-721-362-65	Sequence 65, Appl
79	3	27.3	11	4	US-09-500-124-284	Sequence 284, App
80	3	27.3	11	4	US-09-837-863-2	Sequence 2, Appli
81	3	27.3	11	4	US-09-839-666-12	Sequence 12, Appl
82	3	27.3	11	4	US-09-736-743A-2	Sequence 2, Appli
83	3	27.3	11	4	US-08-843-076D-48	Sequence 48, Appl
84	3	27.3	11	4	US-09-660-742-1	Sequence 1, Appli
85	3	27.3	11	4	US-09-007-288E-89	Sequence 89, Appl
86	3	27.3	11	4	US-09-434-345-2	Sequence 2, Appli
87	3	27.3	11	4	US-09-579-664B-33	Sequence 33, Appl
88	3	27.3	11	4	US-09-632-287A-22	Sequence 22, Appl
89	3	27.3	11	4	US-09-451-067-74	Sequence 74, Appl
90	3	27.3	11	4	US-09-839-542B-3110	Sequence 3110, Ap
91	3	27.3	11	4	US-09-839-542B-3155	Sequence 3155, Ap
92	3	27.3	11	4	US-09-839-542B-3200	Sequence 3200, Ap
93	3	27.3	11	4	US-09-839-542B-3245	Sequence 3245, Ap
94	3	27.3	11	4	US-09-839-542B-3290	Sequence 3290, Ap
95	3	27.3	11	4	US-09-839-542B-3341	Sequence 3341, Ap
96	3	27.3	11	4	US-09-839-542B-3383	Sequence 3383, Ap
97	3	27.3	11	4	US-09-839-542B-3425	Sequence 3425, Ap
98	3	27.3	11	4	US-09-839-542B-3467	Sequence 3467, Ap
99	3	27.3	11	4	US-09-839-542B-3509	Sequence 3509, Ap
100	3	27.3	11	4	US-09-941-611-3	Sequence 3, Appli

## ALIGNMENTS

### RESULT 1

US-08-185-448-5

; Sequence 5, Application US/08185448  
; Patent No. 5580747  
; GENERAL INFORMATION:  
; APPLICANT: SHULTZ, JOHN W.  
; APPLICANT: WHITE, DOUGLAS H.  
; TITLE OF INVENTION: NON-RADIOACTIVE KINASE,  
; TITLE OF INVENTION: PHOSPHATASE AND PROTEASE ASSAY  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL  
; STREET: 100 E. WISCONSIN AVENUE, SUITE 1100  
; CITY: MILWAUKEE  
; STATE: WISCONSIN  
; COUNTRY: USA  
; ZIP: 53202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

;  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version  
; SOFTWARE: #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/185,448  
; FILING DATE: 21-JAN-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/791,928  
; FILING DATE: 12-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SARA, CHARLES S  
; REGISTRATION NUMBER: 30492  
; REFERENCE/DOCKET NUMBER: F.3347-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (608) 255-2022  
; TELEFAX: (608) 255-2182  
; TELEX: 26832 ANDSTARK  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Binding-site  
; LOCATION: 1  
; OTHER INFORMATION: /label= LABEL  
; OTHER INFORMATION: /note= "LOCATION OF LISSAMINE RHODAMINE  
; OTHER INFORMATION: DETECTION TAG"  
US-08-185-448-5

Query Match 36.48; Score 4; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 RQRK 8  
      ||||  
Db 3 RQRK 6

RESULT 2  
US-08-476-405A-10  
; Sequence 10, Application US/08476405A  
; Patent No. 5776459  
; GENERAL INFORMATION:  
; APPLICANT: Vandenbark, Arthur A.  
; TITLE OF INVENTION: Method of Treatment Using TCR VBeta5 Peptides  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Connective Therapeutics, Inc.  
; STREET: 3400 West Bayshore Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94303  
; COMPUTER READABLE FORM:

;  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;  
CURRENT APPLICATION DATA:  
;  
APPLICATION NUMBER: US/08/476,405A  
;  
FILING DATE:  
;  
CLASSIFICATION: 424  
;  
PRIOR APPLICATION DATA:  
;  
APPLICATION NUMBER: US 08/059,020  
;  
FILING DATE: 16-MAR-1993  
;  
PRIOR APPLICATION DATA:  
;  
APPLICATION NUMBER: US 07/735,612  
;  
FILING DATE: 16-JUL-1991  
;  
PRIOR APPLICATION DATA:  
;  
APPLICATION NUMBER: US 07/708,022  
;  
FILING DATE: 31-MAY-1991  
;  
PRIOR APPLICATION DATA:  
;  
APPLICATION NUMBER: US 07/554,529  
;  
FILING DATE: 19-JUL-1990  
;  
PRIOR APPLICATION DATA:  
;  
APPLICATION NUMBER: US 07/467,577  
;  
FILING DATE: 19-JAN-1990  
;  
PRIOR APPLICATION DATA:  
;  
APPLICATION NUMBER: US 07/382,804  
;  
FILING DATE: 19-JUL-1989  
;  
ATTORNEY/AGENT INFORMATION:  
;  
NAME: Lowin, David A.  
;  
REGISTRATION NUMBER: 29,326  
;  
REFERENCE/DOCKET NUMBER: 886 P15  
;  
TELECOMMUNICATION INFORMATION:  
;  
TELEPHONE: 415-843-2800  
;  
TELEFAX: 415-843-2899  
;  
INFORMATION FOR SEQ ID NO: 10:  
;  
SEQUENCE CHARACTERISTICS:  
;  
LENGTH: 11 amino acids  
;  
TYPE: amino acid  
;  
STRANDEDNESS: single  
;  
TOPOLOGY: linear  
;  
MOLECULE TYPE: peptide  
US-08-476-405A-10

Query Match 36.4%; Score 4; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ERQR 7  
|||  
Db 7 ERQR 10

RESULT 3  
US-08-476-405A-11  
;  
Sequence 11, Application US/08476405A  
;  
Patent No. 5776459  
;  
GENERAL INFORMATION:  
;  
APPLICANT: Vandenbark, Arthur A.

; TITLE OF INVENTION: Method of Treatment Using TCR VBeta5 Peptides  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Connective Therapeutics, Inc.  
; STREET: 3400 West Bayshore Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/476,405A  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/059,020  
; FILING DATE: 16-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/735,612  
; FILING DATE: 16-JUL-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/708,022  
; FILING DATE: 31-MAY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/554,529  
; FILING DATE: 19-JUL-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/467,577  
; FILING DATE: 19-JAN-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/382,804  
; FILING DATE: 19-JUL-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lowin, David A.  
; REGISTRATION NUMBER: 29,326  
; REFERENCE/DOCKET NUMBER: 886 P15  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-843-2800  
; TELEFAX: 415-843-2899  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-476-405A-11

Query Match 36.4%; Score 4; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

||||  
7 ERQR 10

RESULT 4  
US-08-747-137-63  
; Sequence 63, Application US/08747137  
; Patent No. 5945033  
; GENERAL INFORMATION:  
; APPLICANT: YEN, Richard C.K.  
; TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR  
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE  
; NUMBER OF SEQUENCES: 184  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/747,137  
; FILING DATE: 12-NOV-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/212,546  
; FILING DATE: 14-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/069,831  
; FILING DATE: 01-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/959,560  
; FILING DATE: 13-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/641,720  
; FILING DATE: 15-JAN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 016197-000840US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
US-08-747-137-63

Query Match 36.4%; Score 4; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQRK 8  
||||  
Db 3 RQRK 6

RESULT 5

US-09-100-930A-10

; Sequence 10, Application US/09100930A  
; Patent No. 6248549  
; GENERAL INFORMATION:  
; APPLICANT: Van Eyk, Jennifer E.  
; APPLICANT: Mak, Alan S.  
; APPLICANT: Cote, Graham P.  
; TITLE OF INVENTION: Methods of Modulating Muscle Contraction  
; FILE REFERENCE: 1997-021-03US  
; CURRENT APPLICATION NUMBER: US/09/100,930A  
; CURRENT FILING DATE: 1998-06-22  
; PRIOR APPLICATION NUMBER: 60/050,478  
; PRIOR FILING DATE: 1997-06-23  
; PRIOR APPLICATION NUMBER: 60/089,505  
; PRIOR FILING DATE: 1998-06-16  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(11)  
; OTHER INFORMATION: Residues 423 to 433 of chicken gizzard caldesmon  
; NAME/KEY: PEPTIDE  
; LOCATION: (11)  
; OTHER INFORMATION: Targeted Ser phospho-amino acid

US-09-100-930A-10

Query Match 36.4%; Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKE 4  
||||  
Db 7 AKKE 10

RESULT 6

US-08-193-521-18

; Sequence 18, Application US/08193521  
; Patent No. 5470950  
; GENERAL INFORMATION:  
; APPLICANT: Maloy, W. Lee  
; APPLICANT: Kari, U. Prasad  
; APPLICANT: Williams, Jon I.  
; TITLE OF INVENTION: Biologically Active Peptide  
; TITLE OF INVENTION: Compositions and Uses Therefor

; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,  
; ADDRESSEE: Cecchi & Stewart  
; STREET: 6 Becker Farm Road  
; CITY: Roseland  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch diskette  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: DW4.V2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/193,521  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/870,960  
; FILING DATE:  
; APPLICATION NUMBER: 07/760,054  
; FILING DATE: 13-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Olstein, Elliot M.  
; REGISTRATION NUMBER: 24,025  
; REFERENCE/DOCKET NUMBER: 421250-161  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: May be a C-terminal amide,  
; OTHER INFORMATION: and/or may be acetylated at  
; OTHER INFORMATION: N-terminus.  
US-08-193-521-18

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 1 AKK 3

RESULT 7  
US-08-197-793-8  
; Sequence 8, Application US/08197793  
; Patent No. 5510461  
; GENERAL INFORMATION:

; APPLICANT: Meuer, S.  
; APPLICANT: Schraven, B.  
; APPLICANT: Schoenhaut, D.  
; APPLICANT: Ratnofsky, S.  
; TITLE OF INVENTION: pp32: A Newly Identified CD45-Associated  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 STATE STREET, SUITE 510  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/197,793  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/688,019;  
; FILING DATE: 19-APR-1991  
; APPLICATION NUMBER: 08/004,199  
; FILING DATE: 13-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A., Jr.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: BBI-006CNCP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-08-197-793-8

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ERQ 6  
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Db 9 ERQ 11

RESULT 8  
US-08-116-733-32  
; Sequence 32, Application US/08116733  
; Patent No. 5516632  
; GENERAL INFORMATION:

; APPLICANT: PALKER, Thomas J.  
; APPLICANT: HAYNES, Barton F.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/116,733  
; FILING DATE: 07-SEP-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WILSON, MARY J.  
; REGISTRATION NUMBER: 32,955  
; REFERENCE/DOCKET NUMBER: 1579-33  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4000  
; TELEFAX: (703) 816-4100  
; TELEX: 200797 NIXN UR  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-116-733-32

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
    |||  
Db 2 AKK 4

RESULT 9  
US-08-329-151-26  
; Sequence 26, Application US/08329151  
; Patent No. 5604203  
; GENERAL INFORMATION:  
; APPLICANT: Balasubramaniam, A.  
; TITLE OF INVENTION: ANALOGS OF PEPTIDE YY AND USES  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street

;  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 50Z or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/329,151  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/038,534  
; FILING DATE: 3/29/93  
; APPLICATION NUMBER: 08/109,326  
; FILING DATE: 08/19/93  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul T. Clark  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00537/105001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11  
; TYPE: amino acid  
; STRANDEDNESS: N/A  
; TOPOLOGY: linear  
; FEATURE:  
; OTHER INFORMATION: The sequence has an acetylated N-terminus  
; OTHER INFORMATION: (i.e., N-`-Ac), rather than an amino N-terminus  
(i.e., H2N-).  
; OTHER INFORMATION: has an amide C-terminus (i.e., CO-NH2), rather than a  
carboxyl  
; OTHER INFORMATION: (i.e., CO-OH).  
US-08-329-151-26

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 8 RQR 10

RESULT 10  
US-08-306-546C-25  
; Sequence 25, Application US/08306546C  
; Patent No. 5605797  
; GENERAL INFORMATION:  
; APPLICANT: Friderici, Karen  
; APPLICANT: Jones, Margaret

; APPLICANT: Chen, Hong  
; APPLICANT: Cavanagh, Kevin  
; TITLE OF INVENTION: Bovine Beta-Mannosidase Gene and Methods  
; TITLE OF INVENTION: of Use  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
; STREET: P.O. Box 828  
; CITY: Bloomfield Hills  
; STATE: Michigan  
; COUNTRY: USA  
; ZIP: 48303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/306,546C  
; FILING DATE: September 15, 1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, DeAnn F.  
; REGISTRATION NUMBER: 36,683  
; REFERENCE/DOCKET NUMBER: 6550-00003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810) 641-1600  
; TELEFAX: (810) 641-0270  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-306-546C-25

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 8 KDT 10  
|||  
Db 2 KDT 4

RESULT 11  
US-08-434-120-112  
; Sequence 112, Application US/08434120  
; Patent No. 5635479  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Margaret A.  
; APPLICANT: Jacob, Leonard S.  
; APPLICANT: Maloy, W. Lee  
; TITLE OF INVENTION: Treatment of Gynecological  
; TITLE OF INVENTION: Malignancies with  
; TITLE OF INVENTION: Biologically Active Peptides  
; NUMBER OF SEQUENCES: 117

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,  
ADDRESSEE: Cecchi & Stewart  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: DW4.V2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/434,120  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/297,950  
FILING DATE:  
APPLICATION NUMBER: US/08/226,108  
FILING DATE:  
APPLICATION NUMBER: US/07/937,462  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Olstein, Elliot M.  
REGISTRATION NUMBER: 24,025  
REFERENCE/DOCKET NUMBER: 421250-194  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 112:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-434-120-112

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AKK	3
Db	1	AKK	3

RESULT 12  
US-08-486-057B-16  
; Sequence 16, Application US/08486057B  
; Patent No. 5650494  
; GENERAL INFORMATION:  
; APPLICANT: Cerletti, Nico  
; APPLICANT: McMaster, Gary K.  
; APPLICANT: Cox, David

; APPLICANT: Schmitz, Albert  
; APPLICANT: Meyhack, Bernd  
; TITLE OF INVENTION: Process for Refolding Recombinantly  
; TITLE OF INVENTION: Produced TGF-beta-like Proteins  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Henry P. No. 5650494ak  
; STREET: 520 White Plains Road, P.O. Box 2005  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10591-9005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,057B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/201,703  
; FILING DATE: 25-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/960,309  
; FILING DATE: 13-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/621,502  
; FILING DATE: 03-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8927546.5  
; FILING DATE: 06-DEC-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5650494ak, Henry P.  
; REGISTRATION NUMBER: 33200  
; REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 277-5110  
; TELEFAX: (908) 277-4306  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-486-057B-16

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DTQ 11  
|||  
Db 1 DTQ 3

RESULT 13

US-08-465-325-111

; Sequence 111, Application US/08465325  
; Patent No. 5686563  
; GENERAL INFORMATION:  
; APPLICANT: Magainin Pharmaceuticals Inc.  
; APPLICANT: 5110 Campus Drive  
; APPLICANT: Plymouth Meeting, PA 19462  
; TITLE OF INVENTION: Biologically Active Peptides Having  
; TITLE OF INVENTION: N-Terminal Substitutions  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I. Street, N.W. Suite 700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,325  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/184,462  
; FILING DATE: 18-JAN-94  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/891,201  
; FILING DATE: 01-JUN-92  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fordis, Jean B  
; REGISTRATION NUMBER: 32,984  
; REFERENCE/DOCKET NUMBER: 05387.0021-03000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 408-4000  
; TELEFAX: (202) 408-4400  
; INFORMATION FOR SEQ ID NO: 111:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-465-325-111

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||

Db

1 AKK 3

RESULT 14  
US-08-465-325-122  
; Sequence 122, Application US/08465325  
; Patent No. 5686563  
; GENERAL INFORMATION:  
; APPLICANT: Magainin Pharmaceuticals Inc.  
; APPLICANT: 5110 Campus Drive  
; APPLICANT: Plymouth Meeting, PA 19462  
; TITLE OF INVENTION: Biologically Active Peptides Having  
; TITLE OF INVENTION: N-Terminal Substitutions  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I. Street, N.W. Suite 700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,325  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/184,462  
; FILING DATE: 18-JAN-94  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/891,201  
; FILING DATE: 01-JUN-92  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fordis, Jean B  
; REGISTRATION NUMBER: 32,984  
; REFERENCE/DOCKET NUMBER: 05387.0021-03000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 408-4000  
; TELEFAX: (202) 408-4400  
; INFORMATION FOR SEQ ID NO: 122:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-465-325-122

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 7 AKK 9

RESULT 15  
US-08-465-325-123  
; Sequence 123, Application US/08465325  
; Patent No. 5686563  
; GENERAL INFORMATION:  
; APPLICANT: Magainin Pharmaceuticals Inc.  
; APPLICANT: 5110 Campus Drive  
; APPLICANT: Plymouth Meeting, PA 19462  
; TITLE OF INVENTION: Biologically Active Peptides Having  
; TITLE OF INVENTION: N-Terminal Substitutions  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I. Street, N.W. Suite 700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,325  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/184,462  
; FILING DATE: 18-JAN-94  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/891,201  
; FILING DATE: 01-JUN-92  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fordis, Jean B  
; REGISTRATION NUMBER: 32,984  
; REFERENCE/DOCKET NUMBER: 05387.0021-03000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 408-4000  
; TELEFAX: (202) 408-4400  
; INFORMATION FOR SEQ ID NO: 123:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-465-325-123

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
|||  
Db 7 AKK 9

RESULT 16

US-08-411-727-10

; Sequence 10, Application US/08411727

; Patent No. 5705161

; Patent No. 5705161 5683703

; GENERAL INFORMATION:

; APPLICANT: VAN DER LEY, Peter Andre

; APPLICANT: POOLMAN, Jan Theunis

; APPLICANT: HOOGERHOUT, Peter

; TITLE OF INVENTION: IMMUNOGENIC MENINGOCOCCAL LPS AND OTHER

; TITLE OF INVENTION: MEMBRANE VESICLES AND VACCINE THEREFROM

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: YOUNG & THOMPSON

; STREET: 745 South 23rd Street, Suite 200

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/411,727

; FILING DATE: 01-MAY-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: NL 9201716

; FILING DATE: 02-OCT-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/NL93/00163

; FILING DATE: 30-JUL-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: PATCH, Andrew J.

; REGISTRATION NUMBER: 32925

; REFERENCE/DOCKET NUMBER: BO 38275

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-521-2297

; TELEFAX: 703-685-0573

; TELEX: 248425 EMBON

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-411-727-10

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10  
|||  
Db 3 KDT 5

RESULT 17

US-08-411-727-18

; Sequence 18, Application US/08411727

; Patent No. 5705161

; Patent No. 5705161 5683703

; GENERAL INFORMATION:

; APPLICANT: VAN DER LEY, Peter Andre

; APPLICANT: POOLMAN, Jan Theunis

; APPLICANT: HOOGERHOUT, Peter

; TITLE OF INVENTION: IMMUNOGENIC MENINGOCOCCAL LPS AND OTHER

; TITLE OF INVENTION: MEMBRANE VESICLES AND VACCINE THEREFROM

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: YOUNG & THOMPSON

; STREET: 745 South 23rd Street, Suite 200

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/411,727

; FILING DATE: 01-MAY-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: NL 9201716

; FILING DATE: 02-OCT-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/NL93/00163

; FILING DATE: 30-JUL-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: PATCH, Andrew J.

; REGISTRATION NUMBER: 32925

; REFERENCE/DOCKET NUMBER: BO 38275

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-521-2297

; TELEFAX: 703-685-0573

; TELEX: 248425 EMBON

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-411-727-18

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10  
|||  
Db 3 KDT 5

RESULT 18

US-08-548-540-119

; Sequence 119, Application US/08548540  
; Patent No. 5733731  
; GENERAL INFORMATION:  
; APPLICANT: Schatz, Peter J.  
; APPLICANT: Cull, Millard G.  
; APPLICANT: Miller, Jeff F.  
; APPLICANT: Stemmer, Willem P.C.  
; APPLICANT: Gates, Christian M.  
; TITLE OF INVENTION: Peptide Library and Screening Method  
; NUMBER OF SEQUENCES: 162  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/548,540  
; FILING DATE: 26-OCT-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/290,641  
; FILING DATE: 15-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/963,321  
; FILING DATE: 15-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 16528J-001240US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 119:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-548-540-119

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ERQ 6  
|||  
Db 4 ERQ 6

RESULT 19

US-08-530-524A-25

; Sequence 25, Application US/08530524A  
; Patent No. 5837836  
; GENERAL INFORMATION:  
; APPLICANT: Friderici, Karen  
; APPLICANT: Jones, Margaret  
; APPLICANT: Chen, Hong  
; APPLICANT: Cavanagh, Kevin  
; TITLE OF INVENTION: Bovine Beta-Mannosidase Gene and Methods  
; TITLE OF INVENTION: of Use  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
; STREET: P.O. Box 828  
; CITY: Bloomfield Hills  
; STATE: Michigan  
; COUNTRY: USA  
; ZIP: 48303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/530,524A  
; FILING DATE: September 19, 1995  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, DeAnn F.  
; REGISTRATION NUMBER: 36,683  
; REFERENCE/DOCKET NUMBER: 6550-00003DVA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810) 641-1600  
; TELEFAX: (810) 641-0270  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-530-524A-25

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 8 KDT 10  
|||  
Db 2 KDT 4

RESULT 20

US-08-248-839C-26

; Sequence 26, Application US/08248839C  
; Patent No. 5843702  
; GENERAL INFORMATION:  
; APPLICANT: McConnell, David  
; APPLICANT: Devine, Kevin  
; APPLICANT: O'Kane, Charles  
; TITLE OF INVENTION: A Gene Expression System  
; NUMBER OF SEQUENCES: 185  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5843702o No. 5843702disk of No. 5843702th America, Inc.  
; STREET: 405 Lexington Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10174-6401  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/248,839C  
; FILING DATE: 25-MAY-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gregg, Valeta A.  
; REGISTRATION NUMBER: 35,127  
; REFERENCE/DOCKET NUMBER: 3614.214-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-867-0123  
; TELEFAX: 212-878-9655  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Protein  
US-08-248-839C-26

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 RQR 7  
|||  
Db 9 RQR 11

RESULT 21

US-08-636-176-8

; Sequence 8, Application US/08636176

; Patent No. 5846822

; GENERAL INFORMATION:

; APPLICANT: Meuer, S.

; APPLICANT: Schraven, B.

; APPLICANT: Schoenhaut, D.

; APPLICANT: Ratnofsky, S.

; TITLE OF INVENTION: pp32: A Newly Identified CD45-Associated

; TITLE OF INVENTION: Protein

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 STATE STREET, SUITE 510

; CITY: BOSTON

; STATE: MASSACHUSETTS

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/636,176

; FILING DATE:

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/688,019; 08/004,199

; FILING DATE: 19-APR-1991; 13-JAN-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: DeConti, Giulio A., Jr.

; REGISTRATION NUMBER: 31,503

; REFERENCE/DOCKET NUMBER: BBI-006CNCP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

US-08-636-176-8

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ERQ 6

|||

Db 9 ERQ 11

RESULT 22  
US-08-737-085A-12  
; Sequence 12, Application US/08737085A  
; Patent No. 5869232  
; GENERAL INFORMATION:  
; APPLICANT: SALLBERG, MATTI  
; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY  
; TITLE OF INVENTION: EXCHANGER  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DARBY & DARBY PC  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/737,085A  
; FILING DATE: 27-DEC-1996  
; CLASSIFICATION: 426  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Green, Reza  
; REGISTRATION NUMBER: 38,475  
; REFERENCE/DOCKET NUMBER: 3846/0C569  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-527-7659  
; TELEFAX: 212-753-6237  
; TELEX: 236687  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-737-085A-12

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QRK 8  
|||  
Db 1 QRK 3

RESULT 23  
US-08-538-960-8

; Sequence 8, Application US/08538960  
; Patent No. 5872230  
; GENERAL INFORMATION:  
; APPLICANT: Stocco, Douglas M.  
; APPLICANT: Clark, Barbara J.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
; TITLE OF INVENTION: REGULATION OF STEROIDOGENESIS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Akin, Gump, Strauss, Hauer & Feld, L.L.P.  
; STREET: 1900 Frost Bank Plaza, 816 Congress Avenue  
; CITY: Austin  
; STATE: TX  
; COUNTRY: U.S.A.  
; ZIP: 78701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/538,960  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mayfield, Denise L.  
; REGISTRATION NUMBER: 33,732  
; REFERENCE/DOCKET NUMBER: 43375.0002/DLM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/499-6200  
; TELEFAX: 512/499-6290  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-538-960-8

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4  
      |||  
Db 9 KKE 11

RESULT 24  
US-08-893-853-54  
; Sequence 54, Application US/08893853  
; Patent No. 5891994  
; GENERAL INFORMATION:  
; APPLICANT: Goldstein, Gideon  
; TITLE OF INVENTION: Methods and Compositions for Impairing  
; TITLE OF INVENTION: Multiplication of HIV-1

; NUMBER OF SEQUENCES: 85  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howson and Howson  
; STREET: Spring House Corporate Cntr., P.O. Box 457  
; CITY: Spring House  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19477  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/893,853  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bak, Mary E.  
; REGISTRATION NUMBER: 31,215  
; REFERENCE/DOCKET NUMBER: GGP2USA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-540-9200  
; TELEFAX: 215-540-5818  
; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-893-853-54

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 2 RQR 4

RESULT 25  
US-08-893-853-74  
; Sequence 74, Application US/08893853  
; Patent No. 5891994  
; GENERAL INFORMATION:  
; APPLICANT: Goldstein, Gideon  
; TITLE OF INVENTION: Methods and Compositions for Impairing  
; TITLE OF INVENTION: Multiplication of HIV-1  
; NUMBER OF SEQUENCES: 85  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howson and Howson  
; STREET: Spring House Corporate Cntr., P.O. Box 457  
; CITY: Spring House  
; STATE: PA  
; COUNTRY: USA

; ZIP: 19477  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/893,853  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bak, Mary E.  
; REGISTRATION NUMBER: 31,215  
; REFERENCE/DOCKET NUMBER: GGP2USA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-540-9200  
; TELEFAX: 215-540-5818  
; INFORMATION FOR SEQ ID NO: 74:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-893-853-74

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 2 RQR 4

RESULT 26  
US-08-466-975A-3  
; Sequence 3, Application US/08466975A  
; Patent No. 5910404  
; GENERAL INFORMATION:  
; APPLICANT: DELEYNS, ROBERT J  
; APPLICANT: POLLET, DIRK  
; APPLICANT: MAERTENS, GEERT  
; APPLICANT: VAN HEUVERSUN, HUGO  
; TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF  
; TITLE OF INVENTION: ANTIBODIES TO HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

;  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,975A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,671  
; FILING DATE:  
; APPLICATION NUMBER: US 07/920,286  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP91/02409  
; FILING DATE: 13-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 90124241.2  
; FILING DATE: 14-DEC-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 7038164000  
; TELEFAX: 7038164100  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-466-975A-3

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QRK 8  
|||  
Db 1 QRK 3

RESULT 27  
US-08-391-671A-3  
; Sequence 3, Application US/08391671A  
; Patent No. 5922532  
; GENERAL INFORMATION:  
; APPLICANT: DELEYNS, ROBERT J  
; APPLICANT: POLLET, DIRK  
; APPLICANT: MAERTENS, GEERT  
; APPLICANT: VAN HEUVERSWUN, HUGO  
; TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF  
; TITLE OF INVENTION: ANTIBODIES TO HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD

;  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,671A  
; FILING DATE: 21-FEB-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/920,286  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP91/02409  
; FILING DATE: 13-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 90124241.2  
; FILING DATE: 14-DEC-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 7038164000  
; TELEFAX: 7038164100  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-391-671A-3

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QRK 8  
      |||  
Db 1 QRK 3

RESULT 28  
US-08-789-588-16  
; Sequence 16, Application US/08789588  
; Patent No. 5922846  
; GENERAL INFORMATION:  
; APPLICANT: Cerletti, Nico  
; APPLICANT: McMaster, Gary K.  
; APPLICANT: Cox, David  
; APPLICANT: Schmitz, Albert  
; APPLICANT: Meyhack, Bernd

; TITLE OF INVENTION: Process for Refolding Recombinantly  
; TITLE OF INVENTION: Produced TGF-beta-like Proteins  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Henry P. No. 5922846ak  
; STREET: 520 White Plains Road, P.O. Box 2005  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10591-9005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/789,588  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/486,057  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/201,703  
; FILING DATE: 25-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/960,309  
; FILING DATE: 13-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/621,502  
; FILING DATE: 03-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8927546.5  
; FILING DATE: 06-DEC-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5922846ak, Henry P.  
; REGISTRATION NUMBER: 33200  
; REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 277-5110  
; TELEFAX: (908) 277-4306  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-789-588-16

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DTQ 11  
|||  
Db 1 DTQ 3

RESULT 29  
US-08-760-075A-1  
; Sequence 1, Application US/08760075A  
; Patent No. 5942429  
; GENERAL INFORMATION:  
; APPLICANT: KIRSCHBAUM, Bernd  
; APPLICANT: MUELLNER, Stefan  
; APPLICANT: BARTLETT, Robert  
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/760,075A  
; FILING DATE: 04-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 19545126.0  
; FILING DATE: 04-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GRANADOS, Patricia D.  
; REGISTRATION NUMBER: 33,683  
; REFERENCE/DOCKET NUMBER: 18748/309  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-760-075A-1  
Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 KKE 4  
Db 9 KKE 11

RESULT 30  
US-08-706-741B-54

; Sequence 54, Application US/08706741B  
; Patent No. 5955593  
; GENERAL INFORMATION:  
; APPLICANT: KORSMAYER, STANLEY J.  
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAVERKAMP, L.C.  
; STREET: 7733 FORSYTH BLVD., SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: USA  
; ZIP: 63146  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/706,741B  
; FILING DATE: 09-SEP-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 965017  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-706-741B-54

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 31  
US-08-924-695A-54  
; Sequence 54, Application US/08924695A  
; Patent No. 5998583  
; GENERAL INFORMATION:  
; APPLICANT: KORSMAYER, STANLEY J.  
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAVERKAMP, L.C.

;  
; STREET: 7733 FORSYTH BLVD., SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/924,695A  
; FILING DATE: 09-SEP-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 971798  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-924-695A-54

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 32  
US-08-467-902A-3  
; Sequence 3, Application US/08467902A  
; Patent No. 6007982  
; GENERAL INFORMATION:  
; APPLICANT: DELEYNS, ROBERT J  
; APPLICANT: POLLET, DIRK  
; APPLICANT: MAERTENS, GEERT  
; APPLICANT: VAN HEUVERSUN, HUGO  
; TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF  
; TITLE OF INVENTION: ANTIBODIES TO HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA

;  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,902A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,671  
; FILING DATE:  
; APPLICATION NUMBER: US 07/920,286  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP91/02409  
; FILING DATE: 13-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 90124241.2  
; FILING DATE: 14-DEC-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 7038164000  
; TELEFAX: 7038164100  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-467-902A-3

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QRK 8  
      |||  
Db 1 QRK 3

RESULT 33  
US-09-246-258-12  
; Sequence 12, Application US/09246258  
; Patent No. 6040137  
; GENERAL INFORMATION:  
; APPLICANT: SALLBERG, MATTI  
; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY  
; TITLE OF INVENTION: EXCHANGER  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DARBY & DARBY PC

;  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/246,258  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/737,085  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Green, Reza  
; REGISTRATION NUMBER: 38,475  
; REFERENCE/DOCKET NUMBER: 3846/OC569  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-527-7659  
; TELEFAX: 212-753-6237  
; TELEX: 236687  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-246-258-12

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QRK 8  
      |||  
Db 1 QRK 3

RESULT 34

US-09-188-579-65

;  
; Sequence 65, Application US/09188579B  
; Patent No. 6107040  
; GENERAL INFORMATION:  
; APPLICANT: Shuman, Stewart  
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation  
; FILE REFERENCE: D6185  
; CURRENT APPLICATION NUMBER: US/09/188,579B  
; CURRENT FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 114  
; SEQ ID NO 65  
; LENGTH: 11  
; TYPE: PRT

; ORGANISM: vaccinia virus  
;  
; FEATURE:  
; OTHER INFORMATION: Motif V of RNA guanylyltransferase.  
US-09-188-579-65

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4  
|||  
Db 5 KKE 7

RESULT 35

US-08-602-999A-284

; Sequence 284, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 284:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid

;       TOPOLOGY: unknown  
;       MOLECULE TYPE: peptide  
US-08-602-999A-284

Query Match               27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity   100.0%; Pred. No. 2.3e+03;  
Matches    3; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Qy           3 KER 5  
              |||  
Db           9 KER 11

RESULT 36

US-09-113-921-74

; Sequence 74, Application US/09113921

; Patent No. 6193981

; GENERAL INFORMATION:

; APPLICANT: Goldstein, Gideon

; TITLE OF INVENTION: Methods and Compositions for Impairing

; TITLE OF INVENTION: Multiplication of HIV-1

; NUMBER OF SEQUENCES: 124

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Howson and Howson

; STREET: Spring House Corporate Cntr., P.O. Box 457

; CITY: Spring House

; STATE: PA

; COUNTRY: USA

; ZIP: 19477

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/113,921

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/893,853

; FILING DATE: 11-JUL-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Bak, Mary E.

; REGISTRATION NUMBER: 31,215

; REFERENCE/DOCKET NUMBER: GGP2AUSA

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-540-9200

; TELEFAX: 215-540-5818

; INFORMATION FOR SEQ ID NO: 74:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-09-113-921-74

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 2 RQR 4

RESULT 37

US-08-659-254-8

; Sequence 8, Application US/08659254  
; Patent No. 6194555  
; GENERAL INFORMATION:  
; APPLICANT: Stocco, Douglas M.  
; APPLICANT: Clark, Dr. Barbara J.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATION  
; TITLE OF INVENTION: OF STEROIDOGENESIS  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Akin, Gump, Strauss, Hauer & Feld, L.L.P.  
; STREET: 1900 Frost Bank Plaza, 816 Congress Avenue  
; CITY: Austin  
; STATE: TX  
; COUNTRY: U.S.A.  
; ZIP: 78701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/659,254  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/538,960  
; FILING DATE: 04-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mayfield, Denise L.  
; REGISTRATION NUMBER: 33,732  
; REFERENCE/DOCKET NUMBER: 43375.0006  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/499-6200  
; TELEFAX: 512/499-6290  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-659-254-8

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4  
|||  
Db 9 KKE 11

RESULT 38  
US-09-206-059-23  
; Sequence 23, Application US/09206059  
; Patent No. 6201104  
; GENERAL INFORMATION:  
; APPLICANT: MacDonald, Nicholas  
; APPLICANT: Sim, Kim Lee  
; TITLE OF INVENTION: Angiogenesis-Inhibiting Protein Binding Peptides and  
; TITLE OF INVENTION: Proteins and Methods of Use  
; FILE REFERENCE: 05213-0370  
; CURRENT APPLICATION NUMBER: US/09/206,059  
; CURRENT FILING DATE: 1998-12-04  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: binding peptides  
US-09-206-059-23

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKD 9  
|||  
Db 5 RKD 7

RESULT 39  
US-09-208-966-2  
; Sequence 2, Application US/09208966  
; Patent No. 6221355  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/208,966  
; CURRENT FILING DATE: 1998-12-10  
; EARLIER APPLICATION NUMBER: 60/082,402  
; EARLIER FILING DATE: 1998-04-20  
; EARLIER APPLICATION NUMBER: 60/069,012  
; EARLIER FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 11  
; TYPE: PRT

; ORGANISM: human  
US-09-208-966-2

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 40

US-09-208-966-16

; Sequence 16, Application US/09208966  
; Patent No. 6221355  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/208,966  
; CURRENT FILING DATE: 1998-12-10  
; EARLIER APPLICATION NUMBER: 60/082,402  
; EARLIER FILING DATE: 1998-04-20  
; EARLIER APPLICATION NUMBER: 60/069,012  
; EARLIER FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: human

US-09-208-966-16

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 6 RQR 8

RESULT 41

US-09-208-966-52

; Sequence 52, Application US/09208966  
; Patent No. 6221355  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/208,966  
; CURRENT FILING DATE: 1998-12-10  
; EARLIER APPLICATION NUMBER: 60/082,402  
; EARLIER FILING DATE: 1998-04-20  
; EARLIER APPLICATION NUMBER: 60/069,012  
; EARLIER FILING DATE: 1997-12-10

; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 52  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: human  
US-09-208-966-52

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 42

US-08-647-405B-6

; Sequence 6, Application US/08647405B  
; Patent No. 6228654  
; GENERAL INFORMATION:  
; APPLICANT: Chait, Brian T.  
; APPLICANT: Zhao, Yingming  
; APPLICANT: Kent, Stephen B.H.  
; TITLE OF INVENTION: METHODS FOR STRUCTURE ANALYSIS OF OLIGOSACCHARIDES  
; FILE REFERENCE: Oligosaccharides  
; CURRENT APPLICATION NUMBER: US/08/647,405B  
; CURRENT FILING DATE: 1996-05-09  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Related to  
; OTHER INFORMATION: human translationally controlled tumor protein  
US-08-647-405B-6

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10  
|||  
Db 4 KDT 6

RESULT 43

US-09-177-249-204

; Sequence 204, Application US/09177249  
; Patent No. 6229064  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, Robert L.  
; APPLICANT: Ohad, Nir  
; APPLICANT: Kiyosue, Tomohiro

; APPLICANT: Yadegari, Ramin  
; APPLICANT: Margossian, Linda  
; APPLICANT: Harada, John  
; APPLICANT: Goldberg, Robert B.  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit  
; TITLE OF INVENTION: Development in Plants  
; FILE REFERENCE: 023070-086120US  
; CURRENT APPLICATION NUMBER: US/09/177,249  
; CURRENT FILING DATE: 1998-10-22  
; EARLIER APPLICATION NUMBER: US 09/071,838  
; EARLIER FILING DATE: 1998-05-01  
; NUMBER OF SEQ ID NOS: 324  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 204  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Arabidopsis sp.  
US-09-177-249-204

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKD 9  
      |||  
Db 3 RKD 5

RESULT 44

US-09-315-444-65

; Sequence 65, Application US/09315444A  
; Patent No. 6232070  
; GENERAL INFORMATION:  
; APPLICANT: Shuman, Stewart  
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation  
; FILE REFERENCE: D6185CIP  
; CURRENT APPLICATION NUMBER: US/09/315,444A  
; CURRENT FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: US 09/188,579  
; PRIOR FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 65  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: vaccinia virus  
; FEATURE:  
; OTHER INFORMATION: Motif V of RNA guanylyltransferase.  
US-09-315-444-65

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4  
      |||  
Db 5 KKE 7

RESULT 45  
US-09-532-106-12  
; Sequence 12, Application US/09532106  
; Patent No. 6245895  
; GENERAL INFORMATION:  
;     APPLICANT: SALLBERG, MATTI  
;     TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY  
;                            EXCHANGER  
;     NUMBER OF SEQUENCES: 23  
;     CORRESPONDENCE ADDRESS:  
;     ADDRESSEE: DARBY & DARBY PC  
;     STREET: 805 Third Avenue  
;     CITY: New York  
;     STATE: New York  
;     COUNTRY: USA  
;     ZIP: 10022  
;     COMPUTER READABLE FORM:  
;     MEDIUM TYPE: Diskette  
;     COMPUTER: IBM Compatible  
;     OPERATING SYSTEM: DOS  
;     SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
;     APPLICATION NUMBER: US/09/532,106  
;     FILING DATE: 21-Mar-2000  
; PRIOR APPLICATION DATA:  
;     APPLICATION NUMBER: US/08/737,085A  
;     FILING DATE: 27-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
;     NAME: Green, Reza  
;     REGISTRATION NUMBER: 38,475  
;     REFERENCE/DOCKET NUMBER: 3846/0C569  
; TELECOMMUNICATION INFORMATION:  
;     TELEPHONE: 212-527-7659  
;     TELEFAX: 212-753-6237  
;     TELEX: 236687  
; INFORMATION FOR SEQ ID NO: 12:  
;     SEQUENCE CHARACTERISTICS:  
;     LENGTH: 11 amino acids  
;     TYPE: amino acid  
;     STRANDEDNESS: single  
;     TOPOLOGY: linear  
;     MOLECULE TYPE: peptide  
;     SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-532-106-12

Query Match                   27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity   100.0%; Pred. No. 2.3e+03;  
Matches   3; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy           6 QRK 8  
              |||  
Db           1 QRK 3

RESULT 46

US-09-338-546-1  
; Sequence 1, Application US/09338546  
; Patent No. 6251645  
; GENERAL INFORMATION:  
; APPLICANT: KIRSCHBAUM, Bernd  
; APPLICANT: MUELLNER, Stefan  
; APPLICANT: BARTLETT, Robert  
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/338,546  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/760,075  
; FILING DATE: 04-DEC-1996  
; APPLICATION NUMBER: DE 19545126.0  
; FILING DATE: 04-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GRANADOS, Patricia D.  
; REGISTRATION NUMBER: 33,683  
; REFERENCE/DOCKET NUMBER: 18748/309  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-338-546-1

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4  
|||  
Db 9 KKE 11

RESULT 47  
US-09-142-732-6

; Sequence 6, Application US/09142732  
; Patent No. 6252045  
; GENERAL INFORMATION:  
; APPLICANT: James M. Anderson  
; APPLICANT: Christina M. Van Itallie  
; TITLE OF INVENTION: Human Occludin, Its Uses and  
; TITLE OF INVENTION: Enhancement of Drug Absorption Using Occludin  
Inhibitors  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Yale University Medical School  
; ADDRESSEE: Section of Digestive Diseases  
; ADDRESSEE: Department of Internal Medicine  
; STREET: 333 Cedar Street, LCI 105  
; CITY: New Haven  
; STATE: Connecticut  
; COUNTRY: United States of America  
; ZIP: 06520-8057  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" 1.44 Mb diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: MS DOS  
; SOFTWARE: Word Processing  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/142,732  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US97/05809  
; FILING DATE: March 14, 1997  
; APPLICATION NUMBER: U.S. 60/013,625  
; FILING DATE: March 15, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mary M. Krinsky  
; REGISTRATION NUMBER: 32423  
; REFERENCE/DOCKET NUMBER: 1751-P0016B.PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 203-324-6155  
; TELEFAX: 203-327-1096  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
; DESCRIPTION: peptide  
; FRAGMENT TYPE: synthetic peptide  
; FEATURE:  
; OTHER INFORMATION: construct used in experi-  
; OTHER INFORMATION: ments

US-09-142-732-6

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKD 9  
|||  
Db 7 RKD 9

RESULT 48  
US-09-044-411-1  
; Sequence 1, Application US/09044411A  
; Patent No. 6258774  
; GENERAL INFORMATION:  
; APPLICANT: Stein, Stanley  
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC  
; FILE REFERENCE: 601-1-083  
; CURRENT APPLICATION NUMBER: US/09/044,411A  
; CURRENT FILING DATE: 1998-03-19  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; FEATURE:  
; OTHER INFORMATION: Internal sequence from the Tat protein, but with  
; OTHER INFORMATION: an extra Cys not found in natural protein.  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (10)  
; OTHER INFORMATION: Xaa is either Cys(biotin) or Lys(biotin) at this  
; OTHER INFORMATION: position.  
; FEATURE:  
; NAME/KEY: BINDING  
; LOCATION: (10)  
; OTHER INFORMATION: Either Cys(biotin) or Lys(biotin) at this  
; OTHER INFORMATION: position.  
; FEATURE:  
; OTHER INFORMATION: Peptide has an N-terminal carboxylic acid residue.  
; FEATURE:  
; OTHER INFORMATION: Peptide has a C-terminal amide group.  
US-09-044-411-1

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 5 RQR 7

RESULT 49  
US-09-044-411-2  
; Sequence 2, Application US/09044411A  
; Patent No. 6258774  
; GENERAL INFORMATION:  
; APPLICANT: Stein, Stanley  
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC  
; FILE REFERENCE: 601-1-083

; CURRENT APPLICATION NUMBER: US/09/044,411A  
; CURRENT FILING DATE: 1998-03-19  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; FEATURE:  
; OTHER INFORMATION: Internal sequence from the Tat protein, but with  
; OTHER INFORMATION: two extra Cys residues not found in the natural  
; OTHER INFORMATION: protein.  
; FEATURE:  
; NAME/KEY: BINDING  
; LOCATION: (10)  
; OTHER INFORMATION: Cys(biotin)  
; FEATURE:  
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.  
; FEATURE:  
; OTHER INFORMATION: Peptide has a C-terminal amide group.  
US-09-044-411-2

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 5 RQR 7

RESULT 50  
US-09-044-411-3  
; Sequence 3, Application US/09044411A  
; Patent No. 6258774  
; GENERAL INFORMATION:  
; APPLICANT: Stein, Stanley  
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC  
; FILE REFERENCE: 601-1-083  
; CURRENT APPLICATION NUMBER: US/09/044,411A  
; CURRENT FILING DATE: 1998-03-19  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; FEATURE:  
; OTHER INFORMATION: Internal sequence from the Tat protein, but with  
; OTHER INFORMATION: an extra Lys and an extra Cys not found in the  
; OTHER INFORMATION: natural protein.  
; FEATURE:  
; NAME/KEY: BINDING  
; LOCATION: (10)  
; OTHER INFORMATION: Lys(biotin)  
; FEATURE:  
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.

; FEATURE:  
; OTHER INFORMATION: Peptide has a C-terminal amide group.  
US-09-044-411-3

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 5 RQR 7

RESULT 51

US-09-044-411-4

; Sequence 4, Application US/09044411A  
; Patent No. 6258774  
; GENERAL INFORMATION:  
; APPLICANT: Stein, Stanley  
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC  
; FILE REFERENCE: 601-1-083  
; CURRENT APPLICATION NUMBER: US/09/044,411A  
; CURRENT FILING DATE: 1998-03-19  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; FEATURE:  
; OTHER INFORMATION: Internal sequence from the Tat protein, but with  
; OTHER INFORMATION: two extra Cys not found in the natural protein.  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (10)  
; OTHER INFORMATION: Cys is the D isomer at this position.  
; FEATURE:  
; NAME/KEY: BINDING  
; LOCATION: (10)  
; OTHER INFORMATION: D-Cys(biotin)  
; FEATURE:  
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.  
; FEATURE:  
; OTHER INFORMATION: Peptide has a C-terminal amide group.

US-09-044-411-4

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 5 RQR 7

RESULT 52

US-09-044-411-5

; Sequence 5, Application US/09044411A  
; Patent No. 6258774  
; GENERAL INFORMATION:  
; APPLICANT: Stein, Stanley  
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC  
; FILE REFERENCE: 601-1-083  
; CURRENT APPLICATION NUMBER: US/09/044,411A  
; CURRENT FILING DATE: 1998-03-19  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; FEATURE:  
; OTHER INFORMATION: Internal sequence from the Tat protein, but with  
; OTHER INFORMATION: an extra Lys and an extra Cys not found in the  
; OTHER INFORMATION: natural protein.  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (10)  
; OTHER INFORMATION: Lys is D isomer at this position.  
; FEATURE:  
; NAME/KEY: BINDING  
; LOCATION: (10)  
; OTHER INFORMATION: D-Lys(biotin)  
; FEATURE:  
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.  
; FEATURE:  
; OTHER INFORMATION: Peptide has a C-terminal amide group.  
US-09-044-411-5

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 5 RQR 7

RESULT 53  
US-09-044-411-6  
; Sequence 6, Application US/09044411A  
; Patent No. 6258774  
; GENERAL INFORMATION:  
; APPLICANT: Stein, Stanley  
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC  
; FILE REFERENCE: 601-1-083  
; CURRENT APPLICATION NUMBER: US/09/044,411A  
; CURRENT FILING DATE: 1998-03-19  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1

; FEATURE:  
; OTHER INFORMATION: Same as Sequence ID 3, but with a substitution of  
; Patent No. 6258774  
; OTHER INFORMATION: Arg to Gln.  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (10)  
; OTHER INFORMATION: Lys is the D isomer at this position.  
; FEATURE:  
; NAME/KEY: BINDING  
; LOCATION: (10)  
; OTHER INFORMATION: D-Lys(biotin)  
; FEATURE:  
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.  
; FEATURE:  
; OTHER INFORMATION: Peptide has a C-terminal amide group.  
US-09-044-411-6

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 5 RQR 7

RESULT 54

US-09-044-411-8

; Sequence 8, Application US/09044411A  
; Patent No. 6258774  
; GENERAL INFORMATION:  
; APPLICANT: Stein, Stanley  
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC  
; FILE REFERENCE: 601-1-083  
; CURRENT APPLICATION NUMBER: US/09/044,411A  
; CURRENT FILING DATE: 1998-03-19  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; FEATURE:  
; OTHER INFORMATION: All amino acids in this sequence are D amino acid.  
; FEATURE:  
; NAME/KEY: BINDING  
; LOCATION: (2)  
; OTHER INFORMATION: D-Lys(biotin)  
; FEATURE:  
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.  
; FEATURE:  
; OTHER INFORMATION: Peptide has a C-terminal amide group.  
US-09-044-411-8

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 5 RQR 7

RESULT 55

US-09-133-062D-28

; Sequence 28, Application US/09133062D  
; Patent No. 6258776  
; GENERAL INFORMATION:  
; APPLICANT: Hemmings, Brian A  
; APPLICANT: Millward, Thomas A  
; TITLE OF INVENTION: Calcium Regulated Kinase  
; FILE REFERENCE: 30110  
; CURRENT APPLICATION NUMBER: US/09/133,062D  
; CURRENT FILING DATE: 1998-08-12  
; PRIOR APPLICATION NUMBER: GB 9717089.8  
; PRIOR FILING DATE: 1997-08-12  
; PRIOR APPLICATION NUMBER: GB 9717499.9  
; PRIOR FILING DATE: 1998-08-19  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 28  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:synthetic peptide  
; OTHER INFORMATION: internal peptide

US-09-133-062D-28

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 3 AKK 5

RESULT 56

US-09-133-062D-29

; Sequence 29, Application US/09133062D  
; Patent No. 6258776  
; GENERAL INFORMATION:  
; APPLICANT: Hemmings, Brian A  
; APPLICANT: Millward, Thomas A  
; TITLE OF INVENTION: Calcium Regulated Kinase  
; FILE REFERENCE: 30110  
; CURRENT APPLICATION NUMBER: US/09/133,062D  
; CURRENT FILING DATE: 1998-08-12  
; PRIOR APPLICATION NUMBER: GB 9717089.8  
; PRIOR FILING DATE: 1997-08-12  
; PRIOR APPLICATION NUMBER: GB 9717499.9  
; PRIOR FILING DATE: 1998-08-19

; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:synthetic peptide  
; OTHER INFORMATION: internal peptide  
US-09-133-062D-29

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 3 AKK 5

RESULT 57

US-09-275-265-3

; Sequence 3, Application US/09275265  
; Patent No. 6287761  
; GENERAL INFORMATION:  
; APPLICANT: DELEYS, ROBERT J  
; APPLICANT: POLLET, DIRK  
; APPLICANT: MAERTENS, GEERT  
; APPLICANT: VAN HEUVERSWUN, HUGO  
; TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF  
; TITLE OF INVENTION: ANTIBODIES TO HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/275,265  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,671  
; FILING DATE: 21-FEB-1995  
; APPLICATION NUMBER: US 07/920,286  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP91/02409  
; FILING DATE: 13-DEC-1991  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 90124241.2  
FILING DATE: 14-DEC-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 7038164000  
TELEFAX: 7038164100  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-09-275-265-3

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QRK 8  
|||  
Db 1 QRK 3

RESULT 58

US-09-057-897-8

Sequence 8, Application US/09057897  
Patent No. 6300476  
GENERAL INFORMATION:  
APPLICANT: Lu, Anthony Y.H.  
APPLICANT: Wang, Regina W.  
TITLE OF INVENTION: Anti-Peptide Antibody Against Human  
TITLE OF INVENTION: Cytochrome P450 3A4  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: NJ  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/057,897  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hand, J. Mark  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 19902

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (732)594-3905  
; TELEFAX: (732)594-4720  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-057-897-8

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11  
|||  
Db 7 DTQ 9

RESULT 59

US-09-057-897-13

; Sequence 13, Application US/09057897  
; Patent No. 6300476  
; GENERAL INFORMATION:  
; APPLICANT: Lu, Anthony Y.H.  
; APPLICANT: Wang, Regina W.  
; TITLE OF INVENTION: Anti-Peptide Antibody Against Human  
; TITLE OF INVENTION: Cytochrome P450 3A4  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: US  
; ZIP: 07065-0907  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/057,897  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hand, J. Mark  
; REGISTRATION NUMBER: 36,545  
; REFERENCE/DOCKET NUMBER: 19902  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (732)594-3905  
; TELEFAX: (732)594-4720  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids

; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-057-897-13

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 9 DTQ 11  
|||  
Db 4 DTQ 6

RESULT 60  
US-09-057-897-18  
; Sequence 18, Application US/09057897  
; Patent No. 6300476  
; GENERAL INFORMATION:  
; APPLICANT: Lu, Anthony Y.H.  
; APPLICANT: Wang, Regina W.  
; TITLE OF INVENTION: Anti-Peptide Antibody Against Human  
; TITLE OF INVENTION: Cytochrome P450 3A4  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: US  
; ZIP: 07065-0907  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/057,897  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hand, J. Mark  
; REGISTRATION NUMBER: 36,545  
; REFERENCE/DOCKET NUMBER: 19902  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (732)594-3905  
; TELEFAX: (732)594-4720  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-057-897-18

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DTQ 11  
|||  
Db 1 DTQ 3

RESULT 61

US-09-296-089-37

; Sequence 37, Application US/09296089  
; Patent No. 6303576  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Byers, Stephen  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: BETA-CATENIN MEDIATED GENE EXPRESSION  
; FILE REFERENCE: 100086.411  
; CURRENT APPLICATION NUMBER: US/09/296,089  
; CURRENT FILING DATE: 1999-04-21  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 37  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus

US-09-296-089-37

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 62

US-09-025-596-34

; Sequence 34, Application US/09025596  
; Patent No. 6340463  
; GENERAL INFORMATION:  
; APPLICANT: Mitchell, William M.  
; APPLICANT: Stratton, Charles W.  
; TITLE OF INVENTION: IDENTIFICATION OF ANTIGENIC PEPTIDE  
; TITLE OF INVENTION: SEQUENCES  
; FILE REFERENCE: VDB98-01  
; CURRENT APPLICATION NUMBER: US/09/025,596  
; CURRENT FILING DATE: 1998-02-18  
; EARLIER APPLICATION NUMBER: 08/911,593  
; EARLIER FILING DATE: 1997-08-14  
; EARLIER APPLICATION NUMBER: 60/023,921  
; EARLIER FILING DATE: 1996-08-14  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 34  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
US-09-025-596-34

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 3 AKK 5

RESULT 63

US-09-115-737-111

; Sequence 111, Application US/09115737  
; Patent No. 6348445  
; GENERAL INFORMATION:  
; APPLICANT: U. Prasad Kari  
; Taffy J. Williams  
; Michael McLane  
; TITLE OF INVENTION: Biologically Active Peptides With Reduced  
; Toxicity in Animals and a Method for Preparing Same  
; NUMBER OF SEQUENCES: 156  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; Dunner, L.L.P.  
; STREET: 1300 I Street, N.W. Suite 700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.3  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/115,737  
; FILING DATE: 15-Jul-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/465,330  
; FILING DATE: 05-JUN-1995  
; APPLICATION NUMBER: 08/184,462  
; FILING DATE: 18-JAN-94  
; APPLICATION NUMBER: 07/891,201  
; FILING DATE: 01-JUN-92  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fordis, Jean B  
; REGISTRATION NUMBER: 32,984  
; REFERENCE/DOCKET NUMBER: 05387.0021-06000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 408-4000  
; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 111:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 111:  
US-09-115-737-111

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 1 AKK 3

RESULT 64  
US-09-115-737-122  
; Sequence 122, Application US/09115737  
; Patent No. 6348445  
; GENERAL INFORMATION:  
; APPLICANT: U. Prasad Kari  
; Taffy J. Williams  
; Michael McLane  
; TITLE OF INVENTION: Biologically Active Peptides With Reduced  
; Toxicity in Animals and a Method for Preparing Same  
; NUMBER OF SEQUENCES: 156  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; Dunner, L.L.P.  
; STREET: 1300 I Street, N.W. Suite 700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.3  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/115,737  
; FILING DATE: 15-Jul-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/465,330  
; FILING DATE: 05-JUN-1995  
; APPLICATION NUMBER: 08/184,462  
; FILING DATE: 18-JAN-94  
; APPLICATION NUMBER: 07/891,201  
; FILING DATE: 01-JUN-92  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fordis, Jean B  
; REGISTRATION NUMBER: 32,984

; REFERENCE/DOCKET NUMBER: 05387.0021-06000  
; TELECOMMUNICATION INFORMATION:  
;     TELEPHONE: (202) 408-4000  
;     TELEFAX: (202) 408-4400  
; INFORMATION FOR SEQ ID NO: 122:  
;     SEQUENCE CHARACTERISTICS:  
;         LENGTH: 11 amino acids  
;         TYPE: amino acid  
;         STRANDEDNESS: single  
;         TOPOLOGY: linear  
;     MOLECULE TYPE: peptide  
;     SEQUENCE DESCRIPTION: SEQ ID NO: 122:  
US-09-115-737-122

Query Match                   27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity   100.0%; Pred. No. 2.3e+03;  
Matches   3; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy           1 AKK 3  
              |||  
Db           7 AKK 9

RESULT 65  
US-09-115-737-123  
; Sequence 123, Application US/09115737  
; Patent No. 6348445  
; GENERAL INFORMATION:  
;     APPLICANT: U. Prasad Kari  
;         Taffy J. Williams  
;         Michael McLane  
;     TITLE OF INVENTION: Biologically Active Peptides With Reduced  
;                           Toxicity in Animals and a Method for Preparing Same  
;     NUMBER OF SEQUENCES: 156  
;     CORRESPONDENCE ADDRESS:  
;         ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
;                           Dunner, L.L.P.  
;         STREET: 1300 I Street, N.W. Suite 700  
;         CITY: Washington  
;         STATE: D.C.  
;         COUNTRY: USA  
;         ZIP: 20005-3315  
;     COMPUTER READABLE FORM:  
;         MEDIUM TYPE: Floppy disk  
;         COMPUTER: IBM PC compatible  
;         OPERATING SYSTEM: PC-DOS/MS-DOS  
;         SOFTWARE: PatentIn Release #1.0, Version #1.3  
;     CURRENT APPLICATION DATA:  
;         APPLICATION NUMBER: US/09/115,737  
;         FILING DATE: 15-Jul-1998  
;         CLASSIFICATION: <Unknown>  
;     PRIOR APPLICATION DATA:  
;         APPLICATION NUMBER: 08/465,330  
;         FILING DATE: 05-JUN-1995  
;         APPLICATION NUMBER: 08/184,462  
;         FILING DATE: 18-JAN-94  
;         APPLICATION NUMBER: 07/891,201

;  
; FILING DATE: 01-JUN-92  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fordis, Jean B  
; REGISTRATION NUMBER: 32,984  
; REFERENCE/DOCKET NUMBER: 05387.0021-06000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 408-4000  
; TELEFAX: (202) 408-4400  
; INFORMATION FOR SEQ ID NO: 123:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 123:  
US-09-115-737-123

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 7 AKK 9

RESULT 66  
US-09-187-859-3110  
; Sequence 3110, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C1  
; CURRENT APPLICATION NUMBER: US/09/187,859A  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3110  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence  
US-09-187-859-3110

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10  
|||  
Db 7 KDT 9

RESULT 67

US-09-187-859-3155

; Sequence 3155, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C1  
; CURRENT APPLICATION NUMBER: US/09/187,859A  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3155  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence

US-09-187-859-3155

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10  
|||  
Db 7 KDT 9

RESULT 68

US-09-187-859-3200

; Sequence 3200, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C1  
; CURRENT APPLICATION NUMBER: US/09/187,859A  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3200  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence

US-09-187-859-3200

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10  
|||  
Db 7 KDT 9

RESULT 69

US-09-187-859-3245

; Sequence 3245, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C1  
; CURRENT APPLICATION NUMBER: US/09/187,859A  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3245  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence

US-09-187-859-3245

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10  
|||  
Db 7 KDT 9

RESULT 70

US-09-187-859-3290

; Sequence 3290, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C1  
; CURRENT APPLICATION NUMBER: US/09/187,859A  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3290  
; LENGTH: 11

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence  
US-09-187-859-3290

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10  
|||  
Db 7 KDT 9

RESULT 71  
US-09-187-859-3341  
; Sequence 3341, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C1  
; CURRENT APPLICATION NUMBER: US/09/187,859A  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3341  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: Desmocollin cell adhesion recognition sequence  
US-09-187-859-3341

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10  
|||  
Db 7 KDT 9

RESULT 72  
US-09-187-859-3383  
; Sequence 3383, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

; FILE REFERENCE: 100086.407C1  
; CURRENT APPLICATION NUMBER: US/09/187,859A  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3383  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: Desmocollin cell adhesion recognition sequence  
US-09-187-859-3383

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10  
|||  
Db 7 KDT 9

RESULT 73  
US-09-187-859-3425  
; Sequence 3425, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C1  
; CURRENT APPLICATION NUMBER: US/09/187,859A  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3425  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: Desmocollin cell adhesion recognition sequence  
US-09-187-859-3425

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10  
|||  
Db 7 KDT 9

RESULT 74  
US-09-187-859-3467

; Sequence 3467, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C1  
; CURRENT APPLICATION NUMBER: US/09/187,859A  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3467  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: Desmocollin cell adhesion recognition sequence  
US-09-187-859-3467

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 8 KDT 10  
|||  
Db 7 KDT 9

RESULT 75  
US-09-187-859-3509  
; Sequence 3509, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C1  
; CURRENT APPLICATION NUMBER: US/09/187,859A  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3509  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: Desmocollin cell adhesion recognition sequence  
US-09-187-859-3509

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KDT 10  
|||  
Db 7 KDT 9

Search completed: April 8, 2004, 15:52:06  
Job time : 12.3077 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 8.61538 Seconds  
(without alignments)  
122.816 Million cell updates/sec

Title: US-09-787-443A-2

Perfect score: 11

Sequence: 1 AKKERQRKDTQ 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 226

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : PIR\_78:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	Query				Description
			Match	Length	DB	ID	
1	3	27.3	11	2	PT0217		T-cell receptor be
2	3	27.3	11	2	PD0441		translation elonga
3	2	18.2	11	1	EOOCC		eledoisin - curled
4	2	18.2	11	1	EOOC		eledoisin - musky
5	2	18.2	11	2	A38841		rhodopsin homolog
6	2	18.2	11	2	PQ0682		photosystem I 17.5
7	2	18.2	11	2	B26744		megascoliakinin -
8	2	18.2	11	2	D61033		ranatachakinin D -
9	2	18.2	11	2	S42449		antl protein - pha
10	2	18.2	11	2	JQ0395		hypothetical prote
11	2	18.2	11	2	S66606		quinoline 2-oxidor
12	2	18.2	11	2	S58244		pyrroloquinoline q
13	2	18.2	11	2	B43669		hypothetical prote

14	2	18.2	11	2	PC2372	58K heat shock pro
15	2	18.2	11	2	S33519	probable secreted
16	2	18.2	11	2	PT0081	protein QA300023 -
17	2	18.2	11	2	G61497	seed protein ws-23
18	2	18.2	11	2	S19775	wound-induced prot
19	2	18.2	11	2	S41747	chaperonin 10 homo
20	2	18.2	11	2	A34135	DNA-binding protei
21	2	18.2	11	2	A61512	variant surface gl
22	2	18.2	11	2	A26120	6-phosphofructokin
23	2	18.2	11	2	E57789	gallbladder stone
24	2	18.2	11	2	PT0287	Ig heavy chain CRD
25	2	18.2	11	2	D56979	collagen alpha 1(I
26	2	18.2	11	2	A33571	follistatin - bovi
27	2	18.2	11	2	S78765	ribosomal protein
28	2	18.2	11	2	S54347	tubulin beta chain
29	2	18.2	11	2	A14454	6-phosphofructokin
30	2	18.2	11	2	A61483	pyridoxal kinase (
31	2	18.2	11	2	PN0664	dystrophin-associat
32	2	18.2	11	2	PH1583	Ig H chain V-D-J r
33	2	18.2	11	2	PN0044	protein kinase C i
34	2	18.2	11	2	PH1376	T antigen variant
35	2	18.2	11	2	S53436	beta-D-galactosida
36	2	18.2	11	2	S65377	cytochrome-c oxida
37	2	18.2	11	2	PH0903	T-cell receptor be
38	2	18.2	11	2	PH0904	T-cell receptor be
39	2	18.2	11	2	PH0922	T-cell receptor be
40	2	18.2	11	2	A48973	glucoamylase A1 (E
41	2	18.2	11	2	H84082	hypothetical prote
42	2	18.2	11	4	S19015	hypothetical prote
43	1	9.1	11	1	XAVIBH	bradykinin-potenti
44	1	9.1	11	1	XASNBA	bradykinin-potenti
45	1	9.1	11	1	ECLQ2M	tachykinin II - mi
46	1	9.1	11	1	SPHO	substance P - hors
47	1	9.1	11	1	A60654	substance P - guin
48	1	9.1	11	1	GMROL	leucosulfakinin -
49	1	9.1	11	1	LFTWWE	probable trpEG lea
50	1	9.1	11	2	S66196	alcohol dehydrogen
51	1	9.1	11	2	G42762	proteasome endopep
52	1	9.1	11	2	S68392	H+-transporting tw
53	1	9.1	11	2	A33917	dihydroorotate (EC
54	1	9.1	11	2	B49164	chromogranin-B - r
55	1	9.1	11	2	JN0023	substance P - chic
56	1	9.1	11	2	S32575	ribosomal protein
57	1	9.1	11	2	A40693	transgelin - sheep
58	1	9.1	11	2	S00616	parasporal crystal
59	1	9.1	11	2	C53652	rhlR protein - Pse
60	1	9.1	11	2	S09074	cytochrome P450-4b
61	1	9.1	11	2	A57458	gene Gax protein -
62	1	9.1	11	2	A26930	ermG leader peptid
63	1	9.1	11	2	D60409	kassinin-like pept
64	1	9.1	11	2	F60409	substance P-like p
65	1	9.1	11	2	E60409	substance P-like p
66	1	9.1	11	2	YHRT	morphogenetic neur
67	1	9.1	11	2	YHHU	morphogenetic neur
68	1	9.1	11	2	YHBO	morphogenetic neur
69	1	9.1	11	2	YHXAE	morphogenetic neur
70	1	9.1	11	2	YHJFHY	morphogenetic neur

71	1	9.1	11	2	A61365	phyllokinin - Rohd
72	1	9.1	11	2	S23308	substance P - rain
73	1	9.1	11	2	S23306	substance P - Atla
74	1	9.1	11	2	B60409	kassinin-like pept
75	1	9.1	11	2	C60409	kassinin-like pept
76	1	9.1	11	2	S07203	uperolein - frog (
77	1	9.1	11	2	S07207	Crinia-angiotensin
78	1	9.1	11	2	S07201	physalaemin - frog
79	1	9.1	11	2	A61033	ranatachakinin A -
80	1	9.1	11	2	B58501	24K kidney and bla
81	1	9.1	11	2	D58502	27K bile and gallb
82	1	9.1	11	2	A58502	38K kidney stone p
83	1	9.1	11	2	C58501	42K bile stone pro
84	1	9.1	11	2	F58501	43.5K bile stone p
85	1	9.1	11	2	PQ0231	beta-glucosidase (
86	1	9.1	11	2	S04875	nifS protein - Bra
87	1	9.1	11	2	I41138	acetyl ornithine d
88	1	9.1	11	2	S42587	celF protein - Esc
89	1	9.1	11	2	S35490	type II site-speci
90	1	9.1	11	2	S21127	precorrin methyltr
91	1	9.1	11	2	S70720	trigger factor hom
92	1	9.1	11	2	S33782	acetolactate synth
93	1	9.1	11	2	B39853	LuxC protein - Pho
94	1	9.1	11	2	A58838	hemolysin - Porphy
95	1	9.1	11	2	E60691	phycobilisome 8K l
96	1	9.1	11	2	D60691	phycobilisome 9K l
97	1	9.1	11	2	PC2330	cycloinulooligosac
98	1	9.1	11	2	B41835	translation elonga
99	1	9.1	11	2	S14087	parasporal crystal
100	1	9.1	11	2	A44755	20alpha-hydroxyste

#### ALIGNMENTS

#### RESULT 1

PT0217

T-cell receptor beta chain V-J region (4-1-E.2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 30-May-1997

C;Accession: PT0217

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted in non-obese diabetic mice.

A;Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0217

A;Molecule type: mRNA

A;Residues: 1-11 <NAK>

C;Keywords: T-cell receptor

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DTQ 11

|||

Db 9 DTQ 11

RESULT 2

PD0441

translation elongation factor TU-like protein P43, mitochondrial - mouse  
(fragment)

C;Species: Mus musculus (house mouse)

C;Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 21-Aug-1998

C;Accession: PD0441

R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.  
submitted to JIPID, August 1998

A;Description: Proteome analysis of mouse brain.

A;Reference number: PD0441

A;Accession: PD0441

A;Molecule type: protein

A;Residues: 1-11 <KAW>

A;Experimental source: striatum

C;Keywords: mitochondrion

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3

|||

Db 4 AKK 6

RESULT 3

EOOCC

eleodoisin - curled octopus

C;Species: Eledone cirrosa, Ozaena cirrosa (curled octopus)

C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 20-Mar-1998

C;Accession: B01561; A01561

R;Anastasi, A.; Erspamer, V.

Arch. Biochem. Biophys. 101, 56-65, 1963

A;Title: The isolation and amino acid sequence of eleodoisin, the active  
endecapeptide of the posterior salivary glands of Eledone.

A;Reference number: A01561

A;Accession: B01561

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland;  
secretagogue; vasodilator; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KD 9

||

Db 4 KD 5

RESULT 4

EOOC

eledoisin - musky octopus

C;Species: Eledone moschata, Ozaena moschata (musky octopus)

C;Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 20-Mar-1998

C;Accession: A01561

R;Anastasi, A.; Erspamer, V.

Arch. Biochem. Biophys. 101, 56-65, 1963

A;Title: The isolation and amino acid sequence of eledoisin, the active endecapeptide of the posterior salivary glands of Eledone.

A;Reference number: A01561

A;Accession: A01561

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland; secretagogue; vasodilator; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KD 9

||

Db 4 KD 5

RESULT 5

A38841

rhodopsin homolog - squid (Watasenia scintillans) (fragment)

N;Alternate names: visual pigment protein

C;Species: Watasenia scintillans (sparkling enope)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 31-Oct-1997

C;Accession: A38841

R;Seidou, M.; Kubota, I.; Hiraki, K.; Kito, Y.

Biochim. Biophys. Acta 957, 318-321, 1988

A;Title: Amino acid sequence of the retinal binding site of squid visual pigment.

A;Reference number: PT0063; MUID:89051045; PMID:3191148

A;Accession: A38841

A;Molecule type: protein

A;Residues: 1-11 <SEI>

C;Superfamily: vertebrate rhodopsin

C;Keywords: chromoprotein; retinal

F;3/Binding site: retinal (Lys) (covalent) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2

||

Db 2 AK 3

RESULT 6

PQ0682

photosystem I 17.5K D2 chain - common tobacco (fragment)

C;Species: Nicotiana tabacum (common tobacco)

C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999

C;Accession: PQ0682

R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.

Plant Physiol. 102, 1259-1267, 1993

A;Title: Molecular heterogeneity of photosystem I. psaD, psaE, psaF, psaH and psaL are all present in isoforms in Nicotiana spp.

A;Reference number: PQ0667; MUID:94105345; PMID:8278548

A;Accession: PQ0682

A;Molecule type: protein

A;Residues: 1-11 <OBO>

C;Superfamily: photosystem I chain II

C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4  
||  
Db 7 KE 8

RESULT 7

B26744

megascoliakinin - garden dagger wasp

N;Alternate names: 6-Thr-bradykinin-Lys-Ala

C;Species: Megascolia flavifrons (garden dagger wasp)

C;Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 18-Aug-2000

C;Accession: B26744; A28609

R;Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.

Toxicon 25, 527-535, 1987

A;Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wasp Megascolia flavifrons.

A;Reference number: A94322; MUID:87293024; PMID:3617088

A;Accession: B26744

A;Molecule type: protein

A;Residues: 1-11 <YAS>

R;Nakajima, T.; Piek, T.; Yashuara, T.; Mantel, P.

Toxicon 26, 34, 1988

A;Title: Two kinins isolated from the venom of Megascolia flavifrons.

A;Reference number: A28609

A;Accession: A28609

A;Molecule type: protein

A;Residues: 1-11 <NAK>

C;Superfamily: unassigned animal peptides

C;Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8

||  
Db 9 RK 10

RESULT 8

D61033

ranatachykinin D - bullfrog

C;Species: Rana catesbeiana (bullfrog)

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 18-Aug-2000

C;Accession: D61033; JE0429

R;Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.

Regul. Pept. 42(Suppl.1), S12, 1992

A;Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.

A;Reference number: A61033

A;Accession: D61033

A;Molecule type: protein

A;Residues: 1-11 <KAN>

R;Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.

Biochem. Biophys. Res. Commun. 177, 588-595, 1991

A;Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.

A;Reference number: JE0426; MUID:91254337; PMID:2043143

A;Accession: JE0429

A;Molecule type: protein

A;Residues: 1-11 <KOZ>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; neuropeptide

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ER 5

||

Db 5 ER 6

RESULT 9

S42449

anti protein - phage P7

C;Species: phage P7

C;Date: 07-Sep-1994 #sequence\_revision 26-May-1995 #text\_change 08-Oct-1999

C;Accession: S42449

R;Citron, M.; Schuster, H.

Cell 62, 591-598, 1990

A;Title: The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.

A;Reference number: S42448; MUID:90335968; PMID:1696181

A;Accession: S42449

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-11 <CIT>

A;Cross-references: EMBL:M35139; NID:g215705; PIDN:AAA32437.1; PID:g215707

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3  
||  
Db 2 KK 3

RESULT 10

JQ0395

hypothetical protein (nodb 3' region) - Azorhizobium caulinodans  
N;Alternate names: hypothetical 1.4K protein  
C;Species: Azorhizobium caulinodans  
A;Note: host Sesbania rostrata  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 03-Feb-1994  
C;Accession: JQ0395  
R;Goethals, K.; Gao, M.; Tomekpe, K.; Van Montagu, M.; Holsters, M.  
Mol. Genet. 219, 289-298, 1989  
A;Title: Common nodABC genes in Nod locus 1 of Azorhizobium caulinodans:  
nucleotide sequence and plant-inducible expression.  
A;Reference number: JQ0393; MUID:90136519; PMID:2615763  
A;Accession: JQ0395  
A;Molecule type: DNA  
A;Residues: 1-11 <GOE>  
A;Cross-references: GB:L18897  
A;Experimental source: strain ORS571

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3  
||  
Db 6 KK 7

RESULT 11

S66606

quinoline 2-oxidoreductase alpha chain - Comamonas testosteroni (fragment)  
C;Species: Comamonas testosteroni  
C;Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999  
C;Accession: S66606  
R;Schach, S.; Tshisuaka, B.; Fetzner, S.; Lingens, F.  
Eur. J. Biochem. 232, 536-544, 1995  
A;Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from Comamonas testosteroni 63. The first two enzymes in quinoline and 3-methylquinoline degradation.  
A;Reference number: S66606; MUID:96035889; PMID:7556204  
A;Accession: S66606  
A;Molecule type: protein  
A;Residues: 1-11 <SCH>  
A;Experimental source: strain 63

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2

||  
Db 1 AK 2

RESULT 12

S58244

pyrroloquinoline quinone synthesis C - Pseudomonas fluorescens (fragment)  
C;Species: Pseudomonas fluorescens  
C;Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 08-Oct-1999  
C;Accession: S58244  
R;Schnider, U.; Keel, C.; Defago, G.; Haas, D.  
submitted to the EMBL Data Library, May 1995  
A;Description: Tn5-directed cloning of pqq genes from Pseudomonas fluorescens  
CHAO: their involvement in the production of the antibiotic pyoluteorin.  
A;Reference number: S58239  
A;Accession: S58244  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-11 <SCH>  
A;Cross-references: EMBL:X87299; NID:g929799; PIDN:CAA60734.1; PID:g929806

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10  
||  
Db 3 DT 4

RESULT 13

B43669

hypothetical protein (rhdA 5' region) - Synechococcus sp. (fragment)  
C;Species: Synechococcus sp.  
C;Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 30-Sep-1993  
C;Accession: B43669  
R;Laudenbach, D.E.; Ehrhardt, D.; Green, L.; Grossman, A.  
J. Bacteriol. 173, 2751-2760, 1991  
A;Title: Isolation and characterization of a sulfur-regulated gene encoding a  
periplasmically localized protein with sequence similarity to rhodanese.  
A;Reference number: A43669; MUID:91210163; PMID:1708376  
A;Accession: B43669  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-11 <LAU>  
A;Cross-references: GB:M65244

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2  
||  
Db 6 AK 7

RESULT 14

PC2372

58K heat shock protein groEL [similarity] - *Bacillus cereus* (strain ts-4)  
(fragment)

C;Species: *Bacillus cereus*

C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000

C;Accession: PC2372

R;Matsuno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.

Biosci. Biotechnol. Biochem. 59, 231-235, 1995

A;Title: Identification of DNA-binding proteins changed after induction of sporulation in *Bacillus cereus*.

A;Reference number: PC2369; MUID:95218265; PMID:7766022

A;Accession: PC2372

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <MAS>

C;Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2  
||  
Db 1 AK 2

RESULT 15

S33519

probable secreted protein - *Acholeplasma laidlawii* (fragment)

C;Species: *Acholeplasma laidlawii*

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 22-Oct-1999

C;Accession: S33519

R;Boyer, M.J.; Jarhede, T.K.; Tegman, V.; Wieslander, A.

submitted to the EMBL Data Library, June 1993

A;Description: Sequence regions from *Acholeplasma laidlawii* which restore export of beta-lactamase in *Escherichia coli*.

A;Reference number: S33518

A;Accession: S33519

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <BOY>

A;Cross-references: EMBL:Z22875; NID:g311706; PIDN:CAA80495.1; PID:g311708

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3  
||  
Db 2 KK 3

RESULT 16

PT0081

protein QA300023 - *Arabidopsis thaliana* (fragment)

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 07-Feb-1996 #sequence\_revision 19-Apr-1996 #text\_change 24-Nov-1999  
C;Accession: PT0081  
R;Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.  
submitted to JIPID, December 1995  
A;Description: Two dimensional electrophoresis of plant proteins and  
standardization of the gel patterns.  
A;Reference number: PN0173  
A;Accession: PT0081  
A;Molecule type: protein  
A;Residues: 1-11 <TSU>  
A;Experimental source: Leaf  
C;Keywords: acetylated amino end  
F;1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4  
||  
Db 2 KE 3

RESULT 17  
G61497  
seed protein ws-23 - winged bean (fragment)  
C;Species: Psophocarpus tetragonolobus (winged bean)  
C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994  
C;Accession: G61497  
R;Hirano, H.  
J. Protein Chem. 8, 115-130, 1989  
A;Title: Microsequence analysis of winged bean seed proteins electroblotted from  
two-dimensional gel.  
A;Reference number: A61491; MUID:89351606; PMID:2765119  
A;Accession: G61497  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-11 <HIR>  
C;Keywords: glycoprotein; seed

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2  
||  
Db 1 AK 2

RESULT 18  
S19775  
wound-induced protein - tomato (fragment)  
C;Species: Lycopersicon esculentum (tomato)  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Sep-1997  
C;Accession: S19775  
R;Parsons, B.L.  
submitted to the EMBL Data Library, May 1991

A;Reference number: S19773  
A;Accession: S19775  
A;Molecule type: mRNA  
A;Residues: 1-11 <PAR>  
A;Cross-references: EMBL:X59884; NID:g19323; PID:g19324

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3  
||  
Db 5 KK 6

RESULT 19

S41747  
chaperonin 10 homolog - potato (fragment)  
C;Species: Solanum tuberosum (potato)  
C;Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 07-May-1999  
C;Accession: S41747  
R;Burt, W.J.E.; Leaver, C.J.  
FEBS Lett. 339, 139-141, 1994  
A;Title: Identification of a chaperonin-10 homologue in plant mitochondria.  
A;Reference number: S41747; MUID:94148071; PMID:7906228  
A;Accession: S41747  
A;Molecule type: protein  
A;Residues: 1-11 <BUR>  
A;Experimental source: mitochondrion  
C;Keywords: mitochondrion; molecular chaperone

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TQ 11  
||  
Db 9 TQ 10

RESULT 20

A34135  
DNA-binding protein p - Crithidia fasciculata mitochondrion (fragment)  
C;Species: mitochondrion Crithidia fasciculata  
C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 07-Dec-1999  
C;Accession: A34135  
R;Tittawella, I.  
FEBS Lett. 260, 57-61, 1990  
A;Title: Kinetoplast DNA-aggregating proteins from the parasitic protozoan  
Crithidia fasciculata.  
A;Reference number: A34135  
A;Accession: A34135  
A;Molecule type: protein  
A;Residues: 1-11 <IT>  
C;Genetics:  
A;Genome: mitochondrion  
A;Genetic code: SGC6

C;Keywords: mitochondrion

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8  
||  
Db 8 RK 9

RESULT 21

A61512

variant surface glycoprotein MITat 1.7 - Trypanosoma brucei (fragment)

C;Species: Trypanosoma brucei

C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 07-May-1999

C;Accession: A61512

R;Holder, A.A.; Cross, G.A.M.

Mol. Biochem. Parasitol. 2, 135-150, 1981

A;Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei.

C-terminal location of antigenically cross-reacting carbohydrate moieties.

A;Reference number: A61512; MUID:81172836; PMID:6163983

A;Accession: A61512

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <HOL>

C;Keywords: glycoprotein

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TQ 11  
||  
Db 5 TQ 6

RESULT 22

A26120

6-phosphofructokinase (EC 2.7.1.11) - pig roundworm (fragment)

N;Alternate names: phosphofructokinase; phosphohexokinase

C;Species: Ascaris suum (pig roundworm)

C;Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 28-Apr-1993

C;Accession: A26120

R;Kulkarni, G.; Rao, G.S.J.; Srinivasan, N.G.; Hofer, H.W.; Yuan, P.M.; Harris, B.G.

J. Biol. Chem. 262, 32-34, 1987

A;Title: Ascaris suum phosphofructokinase. Phosphorylation by protein kinase and sequence of the phosphopeptide.

A;Reference number: A26120; MUID:87083467; PMID:3025208

A;Accession: A26120

A;Molecule type: protein

A;Residues: 1-11 <KUL>

C;Keywords: glycolysis; phosphotransferase

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2  
||  
Db 1 AK 2

RESULT 23

E57789

gallbladder stone matrix protein, 25K - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 23-Feb-1996 #sequence\_revision 23-Feb-1996 #text\_change 23-Feb-1996  
C;Accession: E57789  
R;Binette, J.P.; Binette, M.B.  
submitted to the Protein Sequence Database, February 1996  
A;Description: The proteins of gallbladder stones.  
A;Reference number: A57789  
A;Accession: E57789  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-11 <BIN>

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8  
||  
Db 2 RK 3

RESULT 24

PT0287

Ig heavy chain CRD3 region (clone 4-103) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0287  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain  
diversity and joining segments in adult human peripheral blood B lymphocytes.  
A;Reference number: PT0222; MUID:91108337; PMID:1899102  
A;Accession: PT0287  
A;Molecule type: DNA  
A;Residues: 1-11 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TQ 11  
||  
Db 7 TQ 8

RESULT 25

D56979

collagen alpha 1(II) chain - bovine (fragment)

N;Alternate names: collagen alpha 3(XI) chain

C;Species: Bos primigenius taurus (cattle)

C;Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 11-Jul-1997

C;Accession: D56979

R;Wu, J.J.; Eyre, D.R.

J. Biol. Chem. 270, 18865-18870, 1995

A;Title: Structural analysis of cross-linking domains in cartilage type XI collagen. Insights on polymeric assembly.

A;Reference number: A56978; MUID:95370194; PMID:7642541

A;Accession: D56979

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <WUA>

C;Keywords: pyroglutamic acid

F;l/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form 3(XI))

#status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQ 6  
||  
Db 4 RQ 5

RESULT 26

A33571

follistatin - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 30-Sep-1993

C;Accession: A33571

R;Gospodarowicz, D.; Lau, K.

Biochem. Biophys. Res. Commun. 165, 292-298, 1989

A;Title: Pituitary follicular cells secrete both vascular endothelial growth factor and follistatin.

A;Reference number: A33571; MUID:90073725; PMID:2590228

A;Accession: A33571

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <GOS>

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2  
||  
Db 8 AK 9

RESULT 27

S78765

ribosomal protein MRP-S24, mitochondrial - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C;Accession: S78765  
R;Graack, H.R.  
submitted to the Protein Sequence Database, July 1999  
A;Reference number: S78760  
A;Accession: S78765  
A;Molecule type: protein  
A;Residues: 1-11 <GRA>  
C;Keywords: mitochondrion  
F;1-11/Product: ribosomal protein MRP-S24 (fragment) #status experimental <MAT>

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KD 9  
||  
Db 7 KD 8

RESULT 28  
S54347  
tubulin beta chain - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 27-Oct-1995 #sequence\_revision 30-Jan-1998 #text\_change 07-May-1999  
C;Accession: S54347  
R;Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.  
Biochem. J. 306, 551-555, 1995  
A;Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform  
in glial cells.  
A;Reference number: S54343; MUID:95194333; PMID:7887910  
A;Accession: S54347  
A;Molecule type: protein  
A;Residues: 1-11 <OKA>

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KD 9  
||  
Db 1 KD 2

RESULT 29  
A14454  
6-phosphofructokinase (EC 2.7.1.11) - sheep (fragment)  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 28-Apr-1993  
C;Accession: A14454  
R;Fordyce, A.M.; Midwinter, G.G.; Moore, C.H.  
Biochem. Soc. Trans. 7, 721-723, 1979  
A;Title: The N-terminal amino acid sequence of sheep heart phosphofructokinase.  
A;Reference number: A14454; MUID:80004524; PMID:157899  
A;Accession: A14454  
A;Molecule type: protein

A;Residues: 1-11 <FOR>  
C;Keywords: glycolysis; phosphotransferase

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2  
||  
Db 8 AK 9

RESULT 30

A61483

pyridoxal kinase (EC 2.7.1.35) - sheep (fragment)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994

C;Accession: A61483

R;Churchich, J.E.

J. Protein Chem. 9, 613-621, 1990

A;Title: Cleavage of pyridoxal kinase into two structural domains: kinetics of proteolysis monitored by emission anisotropy.

A;Reference number: A61483; MUID:91197387; PMID:2085386

A;Accession: A61483

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <CHU>

C;Keywords: homodimer; phosphotransferase

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QR 7  
||  
Db 10 QR 11

RESULT 31

PN0664

dystrophin-associated glycoprotein A3a-III - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 07-May-1999

C;Accession: PN0664

R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993

A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained in Duchenne muscular dystrophy muscle.

A;Reference number: PN0662; MUID:94156881; PMID:8113213

A;Accession: PN0664

A;Molecule type: protein

A;Residues: 1-11 <YOS>

C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

C;Keywords: glycoprotein; skeletal muscle

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 9 DT 10  
||  
Db 7 DT 8

RESULT 32

PH1583

Ig H chain V-D-J region (wild-type clone 6) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C;Accession: PH1583

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice using a novel quantitative limiting dilution polymerase chain reaction method.

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1583

A;Molecule type: DNA

A;Residues: 1-11 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 RQ 6  
||  
Db 3 RQ 4

RESULT 33

PN0044

protein kinase C inhibitor I - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Oct-1997 #sequence\_revision 29-Oct-1997 #text\_change 23-Jan-1998

C;Accession: PN0044

R;Kato, H.

Kawasaki Igakkaishi 22, 245-259, 1996

A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuroblastoma cells.

A;Reference number: PN0041

A;Accession: PN0044

A;Molecule type: protein

A;Residues: 1-11 <KAT>

A;Experimental source: neuroblastoma cell

C;Comment: The molecular mass is 13,900 and the pI is 6.36. The amino-terminus is blocked.

C;Keywords: brain

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10  
||  
Db 10 DT 11

RESULT 34

PH1376

T antigen variant K-3 - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 11-May-2000

C;Accession: PH1376

R;Lill, N.L.; Judith Tevethia, M.; Hendrickson, W.G.; Tevethia, S.S.  
J. Exp. Med. 176, 449-457, 1992

A;Title: Cytotoxic T lymphocytes (CTL) against a transforming gene product  
select for transformed cells with point mutations within sequences encoding CTL  
recognition epitopes.

A;Reference number: PH1373; MUID:92364547; PMID:1380062

A;Accession: PH1376

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-11 <LIL>

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4  
||  
Db 6 KE 7

RESULT 35

S53436

beta-D-galactosidase - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 01-Aug-1995 #sequence\_revision 15-May-1998 #text\_change 07-May-1999

C;Accession: S53436; S53437

R;Tulsiani, D.R.P.; Skudlarek, M.D.; Araki, Y.; Orgebin-Crist, M.C.  
Biochem. J. 305, 41-50, 1995

A;Title: Purification and characterization of two forms of beta-D-galactosidase  
from rat epididymal luminal fluid: evidence for their role in the modification  
of sperm plasma membrane glycoprotein(s).

A;Reference number: S53436; MUID:95126928; PMID:7826352

A;Accession: S53436

A;Molecule type: protein

A;Residues: 1-11 <TUL>

A;Experimental source: epididymal fluid

A;Note: 84K form

A;Accession: S53437

A;Molecule type: protein

A;Residues: 1-11 <TUW>

A;Experimental source: epididymal fluid

A;Note: 97K form

C;Keywords: glycoprotein

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QR 7  
||  
Db 6 QR 7

RESULT 36

S65377

cytochrome-c oxidase (EC 1.9.3.1) chain VIa-H, cardiac - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 16-Jul-1999

C;Accession: S65377

R;Schaegger, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.

Eur. J. Biochem. 230, 235-241, 1995

A;Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-terminal sequences suggest identity of the fetal heart and the adult liver isoform.

A;Reference number: S65372; MUID:95324529; PMID:7601105

A;Accession: S65377

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <SCH>

C;Keywords: cardiac muscle; heart; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2  
||  
Db 3 AK 4

RESULT 37

PH0903

T-cell receptor beta chain V-D-J region (hybridoma S1C2A6) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997

C;Accession: PH0903

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandebark, A.A.; Wilson, D.B. J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0903

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: myelin basic protein-immunized T-cell

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ER 5  
||

Db 9 ER 10

RESULT 38

PH0904

T-cell receptor beta chain V-D-J region (hybridoma S22C2) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997

C;Accession: PH0904

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental  
allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0904

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: myelin basic protein-immunized T-cell

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TQ 11

||

Db 10 TQ 11

RESULT 39

PH0922

T-cell receptor beta chain V-D-J region (isolate 8) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997

C;Accession: PH0922

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental  
allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0922

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: concanavalin A-activated lymphoblast

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10

||

Db 9 DT 10

RESULT 40

A48973

glucoamylase A1 (EC 3.2.1.-) - Chalara paradoxa (fragment)  
C;Species: Chalara paradoxa  
C;Date: 19-Dec-1993 #sequence\_revision 25-Apr-1997 #text\_change 25-Apr-1997  
C;Accession: A48973  
R;Monma, M.; Kainuma, K.  
Carbohydr. Res. 227, 385-388, 1992  
A;Title: Heterogeneity of the glucoamylase components of the raw-starch-digesting amylase from Chalara paradoxa.  
A;Reference number: A48973; MUID:92361881; PMID:1499035  
A;Accession: A48973  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-11 <MON>  
A;Note: sequence extracted from NCBI backbone (NCBIP:110946)  
C;Keywords: glycosidase; hydrolase

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ER 5  
||  
Db 10 ER 11

RESULT 41  
H84082  
hypothetical protein BH3464 [imported] - Bacillus halodurans (strain C-125)  
C;Species: Bacillus halodurans  
C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
C;Accession: H84082  
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirama, C.; Nakamura, Y.; Ogasawara, N.; Kuhara, S.; Horikoshi, K.  
Nucleic Acids Res. 28, 4317-4331, 2000  
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis.  
A;Reference number: A83650; MUID:20512582; PMID:11058132  
A;Accession: H84082  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-11 <STO>  
A;Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB07183.1;  
GSPDB:GN00137  
A;Experimental source: strain C-125  
C;Genetics:  
A;Gene: BH3464

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4  
||  
Db 4 KE 5

RESULT 42

S19015

hypothetical protein 11 ruvC-yebC intergenic region - Escherichia coli  
C;Species: Escherichia coli  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: S19015  
R;Sharples, G.J.; Lloyd, R.G.  
J. Bacteriol. 173, 7711-7715, 1991  
A;Title: Resolution of Holliday junctions in Escherichia coli: identification of the ruvC gene product as a 19-kilodalton protein.  
A;Reference number: S19013; MUID:92041688; PMID:1657895  
A;Accession: S19015  
A;Molecule type: DNA  
A;Residues: 1-11 <SHA>  
A;Cross-references: EMBL:X59551; NID:g42172; PIDN:CAA42127.1; PID:g42174  
C;Comment: This is the hypothetical translation of a sequence that was not reported as a coding sequence in the complete genome.

Query Match 18.2%; Score 2; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2  
||  
Db 4 AK 5

RESULT 43

XAVIBH

bradykinin-potentiating peptide - halys viper  
N;Alternate names: BPP  
C;Species: Agkistrodon halys (halys viper)  
C;Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 05-Aug-1994  
C;Accession: JC0002  
R;Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.  
Peptides 6, 339-342, 1985  
A;Title: Structure-function studies on the bradykinin potentiating peptide from Chinese snake venom (Agkistrodon halys Pallas).  
A;Reference number: JC0002; MUID:86177022; PMID:3008123  
A;Accession: JC0002  
A;Molecule type: protein  
A;Residues: 1-11 <CHI>  
C;Comment: Because this peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin, it is an antihypertensive agent.  
C;Superfamily: bradykinin-potentiating peptide  
C;Keywords: angiotensin-converting enzyme inhibitor; antihypertensive; bradykinin; pyroglutamic acid; venom  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6  
|  
Db 1 Q 1

RESULT 44

XASNBA

bradykinin-potentiating peptide B - mamushi

C;Species: Agkistrodon blomhoffi (mamushi)

C;Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 08-Dec-1995

C;Accession: A01254

R;Kato, H.; Suzuki, T.

Proc. Jpn. Acad. 46, 176-181, 1970

A;Reference number: A01254

A;Accession: A01254

A;Molecule type: protein

A;Residues: 1-11 <KAT>

A;Note: the sequence of the natural peptide was confirmed by the synthesis and analysis of a peptide having the identical structure and biological properties

C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6  
|  
Db 1 Q 1

RESULT 45

ECLQ2M

tachykinin II - migratory locust

C;Species: Locusta migratoria (migratory locust)

C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 08-Dec-1995

C;Accession: S08266

R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; de Loof, A.

FEBS Lett. 261, 397-401, 1990

A;Title: Locustatachykinin I and II, two novel insect neuropeptides with homology to peptides of the vertebrate tachykinin family.

A;Reference number: S08265; MUID:90184489; PMID:2311766

A;Accession: S08266

A;Molecule type: protein

A;Residues: 1-11 <SCH>

C;Superfamily: tachykinin

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;1/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
|  
Db 1 A 1

RESULT 46

SPHO

substance P - horse  
C;Species: Equus caballus (domestic horse)  
C;Date: 23-Oct-1981 #sequence\_revision 23-Oct-1981 #text\_change 23-Aug-1996  
C;Accession: A01558  
R;Studer, R.O.; Trzeciak, A.; Lergier, W.  
Helv. Chim. Acta 56, 860-866, 1973  
A;Title: Isolierung und Aminosaeuresequenz von Substanz P aus Pferdedarm.  
A;Reference number: A01558  
A;Accession: A01558  
A;Molecule type: protein  
A;Residues: 1-11 <STU>  
C;Superfamily: substance P precursor  
C;Keywords: amidated carboxyl end; hormone  
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5  
|  
Db 1 R 1

RESULT 47

A60654  
substance P - guinea pig  
C;Species: Cavia porcellus (guinea pig)  
C;Date: 14-May-1993 #sequence\_revision 27-Jun-1994 #text\_change 08-Dec-1995  
C;Accession: A60654  
R;Murphy, R.  
Neuropeptides 14, 105-110, 1989  
A;Title: Primary amino acid sequence of guinea-pig substance P.  
A;Reference number: A60654; MUID:90044685; PMID:2478925  
A;Accession: A60654  
A;Molecule type: protein  
A;Residues: 1-11 <MUR>  
C;Superfamily: substance P precursor  
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin  
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5  
|  
Db 1 R 1

RESULT 48

GMROL  
leucosulfakinin - Madeira cockroach  
N;Alternate names: LSK  
C;Species: Leucophaea maderae (Madeira cockroach)  
C;Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 13-Sep-1996

C;Accession: A01622  
R;Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.  
Science 234, 71-73, 1986  
A;Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and cholecystokinin.  
A;Reference number: A01622; MUID:86315858; PMID:3749893  
A;Accession: A01622  
A;Molecule type: protein  
A;Residues: 1-11 <NAC>  
C;Superfamily: gastrin  
C;Keywords: amidated carboxyl end; hormone; sulfoprotein  
F;6/Binding site: sulfate (Tyr) (covalent) #status experimental  
F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4  
|  
Db 1 E 1

RESULT 49  
LFTWWE  
probable trpEG leader peptide - *Thermus aquaticus*  
C;Species: *Thermus aquaticus*  
C;Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 16-Jul-1999  
C;Accession: S03315  
R;Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T.  
Biochim. Biophys. Acta 950, 303-312, 1988  
A;Title: Molecular cloning and nucleotide sequence of *Thermus thermophilus* HB8 trpE and trpG.  
A;Reference number: S03315; MUID:89000781; PMID:2844259  
A;Accession: S03315  
A;Molecule type: DNA  
A;Residues: 1-11 <SAT>  
A;Cross-references: EMBL:X07744; NID:g48261; PIDN:CAA30565.1; PID:g48262  
A;Note: the source is designated as *Thermus thermophilus* HB8  
C;Genetics:  
A;Gene: trpL  
C;Superfamily: probable trpEG leader peptide

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
|  
Db 2 A 2

RESULT 50  
S66196  
alcohol dehydrogenase (EC 1.1.1.1) class III high affinity form - cod (*Gadus* sp.) (fragment)  
C;Species: *Gadus* sp. (cod)

C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 12-Jun-1998

C;Accession: S66196

R;Hjelmqvist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.;  
Hendrickson, R.C.; Michel, H.; Shabanowitz, J.; Hunt, D.F.; Joernvall, H.  
FEBS Lett. 367, 237-240, 1995

A;Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases. Mass-spectrometric analysis of plant, lower vertebrate and higher vertebrate class I, II, and III forms of the enzyme.

A;Reference number: S66191; MUID:95331382; PMID:7607314

A;Accession: S66196

A;Molecule type: protein

A;Residues: 1-11 <HJE>

C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 T 10

|

Db 1 T 1

RESULT 51

G42762

proteasome endopeptidase complex (EC 3.4.25.1) subunit 13 - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Feb-2003

C;Accession: G42762

R;Dick, L.R.; Moomaw, C.R.; Pramanik, B.C.; DeMartino, G.N.; Slaughter, C.A.  
Biochemistry 31, 7347-7355, 1992

A;Title: Identification and localization of a cysteinyl residue critical for the trypsin-like catalytic activity of the proteasome.

A;Reference number: A42762; MUID:92378961; PMID:1510924

A;Accession: G42762

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <DIC>

A;Note: sequence extracted from NCBI backbone (NCBIP:112176)

C;Superfamily: multicatalytic endopeptidase complex chain C9

C;Keywords: hydrolase

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2

|

Db 8 K 8

RESULT 52

S68392

H+-transporting two-sector ATPase (EC 3.6.3.14) chain I - Chlamydomonas reinhardtii chloroplast (fragment)

N;Alternate names: ATP synthase chain I

C;Species: chloroplast Chlamydomonas reinhardtii  
C;Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 03-Jun-2002  
C;Accession: S68392  
R;Fiedler, H.R.; Schmid, R.; Leu, S.; Shavit, N.; Strotmann, H.  
FEBS Lett. 377, 163-166, 1995  
A;Title: Isolation of CF(0)CF(1) from Chlamydomonas reinhardtii cw15 and the N-terminal amino acid sequences of the CF(0)CF(1) subunits.  
A;Reference number: S68388; MUID:96128220; PMID:8543042  
A;Accession: S68392  
A;Molecule type: protein  
A;Residues: 1-11 <FIE>  
A;Experimental source: strain CW15  
C;Genetics:  
A;Genome: chloroplast  
C;Superfamily: H<sup>+</sup>-transporting ATP synthase protein 6  
C;Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; thylakoid

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 E 4  
|  
Db 1 E 1

RESULT 53  
A33917  
dihydroorotate (EC 3.5.2.3) - Chinese hamster (fragment)  
C;Species: Cricetulus griseus (Chinese hamster)  
C;Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 07-Nov-1997  
C;Accession: A33917  
R;Simmer, J.P.; Kelly, R.E.; Scully, J.L.; Grayson, D.R.; Rinker Jr., A.G.;  
Bergh, S.T.; Evans, D.R.  
Proc. Natl. Acad. Sci. U.S.A. 86, 4382-4386, 1989  
A;Title: Mammalian aspartate transcarbamylase (ATCase): sequence of the ATCase domain and interdomain linker in the CAD multifunctional polypeptide and properties of the isolated domain.  
A;Reference number: A33917; MUID:89282776; PMID:2543974  
A;Accession: A33917  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-11 <SIM>  
A;Cross-references: GB:M23652  
C;Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase homology; Bacillus dihydroorotate homology; biotin carboxylase homology; carbamoyl-phosphate synthase (ammonia) homology; carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology; carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology; trpG homology  
C;Keywords: hydrolase

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 E 4

Db 2 E 2

RESULT 54

B49164

chromogranin-B - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 31-Oct-1997

C;Accession: B49164

R;Nielsen, E.; Welinder, B.S.; Madsen, O.D.

Endocrinology 129, 3147-3156, 1991

A;Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides through processing at mono-, di-, or tribasic residues.

A;Reference number: A49164; MUID:92063871; PMID:1954895

A;Accession: B49164

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <NIE>

A;Note: sequence extracted from NCBI backbone (NCBIP:66370)

C;Superfamily: chromogranin B precursor

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4

|

Db 4 E 4

RESULT 55

JN0023

substance P - chicken

C;Species: Gallus gallus (chicken)

C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 11-Jul-1997

C;Accession: JN0023

R;Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.

Regul. Pept. 20, 171-180, 1988

A;Title: [Arg3]substance P and neurokinin A from chicken small intestine.

A;Reference number: JN0023; MUID:88204263; PMID:2452461

A;Accession: JN0023

A;Molecule type: protein

A;Residues: 1-11 <CON>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5

|

Db 1 R 1

RESULT 56

S32575

ribosomal protein S2, plastid - squawroot plastid (fragment)  
C;Species: plastid *Conopholis americana* (squawroot)  
C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 13-Aug-1999  
C;Accession: S32575  
R;Taylor, G.W.; Wolfe, K.H.; Morden, C.W.; dePamphilis, C.W.; Palmer, J.D.  
Curr. Genet. 20, 515-518, 1991  
A;Title: Lack of a functional plastid tRNA(Cys) gene is associated with loss of  
photosynthesis in a lineage of parasitic plants.  
A;Reference number: S32575; MUID:92145776; PMID:1723664  
A;Accession: S32575  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-11 <TAY>  
A;Cross-references: EMBL:X64567; NID:g11275; PIDN:CAA45868.1; PID:g11276  
C;Genetics:  
A;Gene: rps2  
A;Genome: plastid  
C;Superfamily: *Escherichia coli* ribosomal protein S2  
C;Keywords: plastid; protein biosynthesis; ribosome

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4  
|  
Db 11 E 11

RESULT 57

A40693

transgelin - sheep (fragment)  
C;Species: *Ovis orientalis aries*, *Ovis ammon aries* (domestic sheep)  
C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 31-Oct-1997  
C;Accession: A40693  
R;Shapland, C.; Hsuan, J.J.; Totty, N.F.; Lawson, D.  
J. Cell Biol. 121, 1065-1073, 1993  
A;Title: Purification and properties of transgelin: a transformation and shape  
change sensitive actin-gelling protein.  
A;Reference number: A40693; MUID:93273790; PMID:8501116  
A;Accession: A40693  
A;Molecule type: protein  
A;Residues: 1-11 <SHA>  
A;Experimental source: aorta  
C;Comment: This protein gels actin and is down regulated by transformation or  
loss of cell adherence in culture.  
C;Superfamily: smooth muscle protein SM22; calponin repeat homology; smooth  
muscle protein SM22 homology  
C;Keywords: actin binding; cytoskeleton

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2

Db 1 K 1

RESULT 58  
S00616  
parasporal crystal protein, wax moth-specific - *Bacillus thuringiensis* (strain galleriae 11-67) (fragment)  
N;Alternate names: delta-endotoxin; parasporal crystal protein positive chain  
C;Species: *Bacillus thuringiensis*  
C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 13-Sep-1996  
C;Accession: S00616  
R;Chestukhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M.  
FEBS Lett. 232, 249-251, 1988  
A;Title: *Bacillus thuringiensis* ssp. *galleriae* simultaneously produces two delta-endotoxins differing strongly in primary structure and entomocidal activity.  
A;Reference number: S00615  
A;Accession: S00616  
A;Molecule type: protein  
A;Residues: 1-11 <CHE>  
C;Comment: This toxin is effective against the larvae of *Galleria melonella* (greater wax moth) but not those of *Lymantria dispar* (gypsy moth).  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
|  
Db 4 A 4

RESULT 59  
C53652  
rhlR protein - *Pseudomonas aeruginosa* (fragment)  
C;Species: *Pseudomonas aeruginosa*  
C;Date: 21-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 21-Aug-1998  
C;Accession: C53652  
R;Ochsner, U.A.; Fiechter, A.; Reiser, J.  
J. Biol. Chem. 269, 19787-19795, 1994  
A;Title: Isolation, characterization, and expression in *Escherichia coli* of the *Pseudomonas aeruginosa* rhlAB genes encoding a rhamnosyltransferase involved in rhamnolipid biosurfactant synthesis.  
A;Reference number: A53652; MUID:94327521; PMID:8051059  
A;Accession: C53652  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-11 <OCH>  
A;Cross-references: GB:L28170  
C;Superfamily: *sdmA* regulatory protein

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5  
|  
Db 2 R 2

RESULT 60  
S09074  
cytochrome P450-4b - rat (fragment)  
N;Alternate names: cytochrome P450K-5  
N;Contains: oxidoreductase (EC 1.1.1.1)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 23-Apr-1993 #sequence\_revision 23-Apr-1993 #text\_change 05-Mar-1999  
C;Accession: S09074  
R;Imaoka, S.; Terano, Y.; Funae, Y.  
Arch. Biochem. Biophys. 278, 168-178, 1990  
A;Title: Changes in the amount of cytochrome P450s in rat hepatic microsomes with starvation.  
A;Reference number: S09072; MUID:90210577; PMID:2321956  
A;Accession: S09074  
A;Molecule type: protein  
A;Residues: 1-11 <IMA>  
C;Superfamily: unassigned cytochrome P450; cytochrome P450 homology  
C;Keywords: heme; microsome; monooxygenase; oxidoreductase; transmembrane protein

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 T 10  
|  
Db 5 T 5

RESULT 61  
A57458  
gene Gax protein - mouse (fragment)  
C;Species: Mus sp. (mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 15-Oct-1999  
C;Accession: A57458  
R;Andres, V.; Fisher, S.; Wearsch, P.; Walsh, K.  
Mol. Cell. Biol. 15, 4272-4281, 1995  
A;Title: Regulation of Gax homeobox gene transcription by a combination of positive factors including myocyte-specific enhancer factor 2.  
A;Reference number: A57458; MUID:95349593; PMID:7623821  
A;Accession: A57458  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-11 <RES>  
A;Cross-references: GB:S79168; NID:g1050991  
C;Genetics:  
A;Gene: Gax  
C;Superfamily: unassigned homeobox proteins; homeobox homology  
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 9.1%; Score 1; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4  
|  
Db 2 E 2

RESULT 62

A26930

ermG leader peptide 1 - *Bacillus sphaericus*  
C;Species: *Bacillus sphaericus*  
C;Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 24-Sep-1999  
C;Accession: A26930  
R;Monod, M.; Mohan, S.; Dubnau, D.  
J. Bacteriol. 169, 340-350, 1987  
A;Title: Cloning and analysis of ermG, a new macrolide-lincosamide-streptogramin B resistance element from *Bacillus sphaericus*.  
A;Reference number: A91840; MUID:87083389; PMID:3025178  
A;Accession: A26930  
A;Molecule type: DNA  
A;Residues: 1-11 <MON>  
A;Cross-references: GB:MI5332; NID:g142881; PIDN:AAA22417.1; PID:g142882  
C;Superfamily: unassigned leader peptides

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2  
|  
Db 3 K 3

RESULT 63

D60409

kassinin-like peptide K-III - frog (*Pseudophryne guentheri*)  
C;Species: *Pseudophryne guentheri*  
C;Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 02-Sep-2000  
C;Accession: D60409  
R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri, P.; Erspamer, V.  
Peptides 11, 299-304, 1990  
A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog *Pseudophryne guentheri*.  
A;Reference number: A60409; MUID:90287814; PMID:2356157  
A;Accession: D60409  
A;Molecule type: protein  
A;Residues: 1-11 <SIM>  
C;Superfamily: unassigned animal peptides  
C;Keywords: amidated carboxyl end; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6  
|  
Db 1 Q 1

RESULT 64

F60409

substance P-like peptide II - frog (Pseudophryne guentheri)  
C;Species: Pseudophryne guentheri  
C;Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 02-Sep-2000  
C;Accession: F60409  
R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;  
Melchiorri, P.; Erspamer, V.  
Peptides 11, 299-304, 1990  
A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of  
the Australian frog Pseudophryne guentheri.  
A;Reference number: A60409; MUID:90287814; PMID:2356157  
A;Accession: F60409  
A;Molecule type: protein  
A;Residues: 1-11 <SIM>  
C;Superfamily: unassigned animal peptides  
C;Keywords: amidated carboxyl end; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6  
|  
Db 1 Q 1

RESULT 65

E60409

substance P-like peptide I - frog (Pseudophryne guentheri)  
C;Species: Pseudophryne guentheri  
C;Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 02-Sep-2000  
C;Accession: E60409  
R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;  
Melchiorri, P.; Erspamer, V.  
Peptides 11, 299-304, 1990  
A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of  
the Australian frog Pseudophryne guentheri.  
A;Reference number: A60409; MUID:90287814; PMID:2356157  
A;Accession: E60409  
A;Molecule type: protein  
A;Residues: 1-11 <SIM>  
C;Superfamily: unassigned animal peptides  
C;Keywords: amidated carboxyl end; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;

Matches	1;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	6	Q	6						
Db	1	Q	1						

RESULT 66

YHRT

morphogenetic neuropeptide - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000

C;Accession: A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: A01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator by the authors, because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match	9.1%	Score	1;	DB	2;	Length	11;		
Best Local Similarity	100.0%	Pred.	No.	2.1e+05;					
Matches	1;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;

Qy	6	Q	6						
Db	1	Q	1						

RESULT 67

YHHU

morphogenetic neuropeptide - human

C;Species: Homo sapiens (man)

C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000

C;Accession: B01427; A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: B01427  
A;Molecule type: protein  
A;Residues: 1-11 <BOD>  
R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
FEBS Lett. 131, 317-321, 1981  
A;Title: Synthesis of a new neuropeptide, the head activator from hydra.  
A;Reference number: A91296; MUID:82050803; PMID:7297679  
A;Contents: annotation; synthesis  
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity  
C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.  
C;Superfamily: unassigned animal peptides  
C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide  
F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 6 Q 6  
|  
Db 1 Q 1

RESULT 68  
YHBO  
morphogenetic neuropeptide - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C;Accession: C01427; A01427  
R;Bodenmuller, H.; Schaller, H.C.  
Nature 293, 579-580, 1981  
A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.  
A;Reference number: A93266; MUID:82035850; PMID:7290191  
A;Accession: C01427  
A;Molecule type: protein  
A;Residues: 1-11 <BOD>  
R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
FEBS Lett. 131, 317-321, 1981  
A;Title: Synthesis of a new neuropeptide, the head activator from hydra.  
A;Reference number: A91296; MUID:82050803; PMID:7297679  
A;Contents: annotation; synthesis  
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity  
C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.  
C;Superfamily: unassigned animal peptides  
C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide

F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6  
|  
Db 1 Q 1

RESULT 69

YHXAE

morphogenetic neuropeptide - sea anemone (*Anthopleura elegantissima*)

N;Alternate names: head activator

C;Species: *Anthopleura elegantissima*

C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000

C;Accession: A93900; A01427

R;Schaller, H.C.; Bodenmuller, H.

Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.

A;Reference number: A93900

A;Accession: A93900

A;Molecule type: protein

A;Residues: 1-11 <SCH>

R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6  
|  
Db 1 Q 1

RESULT 70

YHJFHY

morphogenetic neuropeptide - *Hydra attenuata*

N;Alternate names: head activator

C;Species: *Hydra attenuata*

C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000

C;Accession: B93900; A01427  
R;Schaller, H.C.; Bodenmuller, H.  
Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981  
A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.  
A;Reference number: A93900  
A;Accession: B93900  
A;Molecule type: protein  
A;Residues: 1-11 <SCH>  
R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
FEBS Lett. 131, 317-321, 1981  
A;Title: Synthesis of a new neuropeptide, the head activator from hydra.  
A;Reference number: A91296; MUID:82050803; PMID:7297679  
A;Contents: annotation; synthesis  
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity  
C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.  
C;Superfamily: unassigned animal peptides  
C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	6	Q	6
Db	1	Q	1

RESULT 71  
A61365  
phyllokinin - Rohde's leaf frog  
N;Alternate names: bradykinyl-isoleucyl-tyrosine O-sulfate  
C;Species: Phylomedusa rohdei (Rohde's leaf frog)  
C;Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 18-Aug-2000  
C;Accession: A61365  
R;Anastasi, A.; Bertaccini, G.; Erspamer, V.  
Br. J. Pharmacol. 27, 479-485, 1966  
A;Title: Pharmacological data on phyllokinin (bradykinyl-isoleucyl-tyrosine O-sulphate) and bradykinyl-isoleucyl-tyrosine.  
A;Reference number: A61365; MUID:67179312; PMID:5970899  
A;Accession: A61365  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-11 <ANA>  
C;Superfamily: unassigned animal peptides  
C;Keywords: sulfoprotein  
F;11/Binding site: sulfate (Tyr) (covalent) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5  
|  
Db 1 R 1

RESULT 72

S23308

substance P - rainbow trout

C;Species: Oncorhynchus mykiss (rainbow trout)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 18-Aug-2000

C;Accession: S23308

R;Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A;Title: Substance-P-related and neuropeptide-A-related peptides from the brain of the cod and trout.

A;Reference number: S23186; MUID:92298992; PMID:1376687

A;Accession: S23308

A;Molecule type: protein

A;Residues: 1-11 <JEN>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A

C;Superfamily: unassigned animal peptides

C;Keywords: neuropeptide; amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2  
|  
Db 1 K 1

RESULT 73

S23306

substance P - Atlantic cod

C;Species: Gadus morhua (Atlantic cod)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 18-Aug-2000

C;Accession: S23306

R;Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A;Title: Substance-P-related and neuropeptide-A-related peptides from the brain of the cod and trout.

A;Reference number: S23186; MUID:92298992; PMID:1376687

A;Accession: S23306

A;Molecule type: protein

A;Residues: 1-11 <JEN>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A  
C;Superfamily: unassigned animal peptides  
C;Keywords: neuropeptide; amidated carboxyl end; tachykinin  
F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2  
|  
Db 1 K 1

RESULT 74

B60409

kassinin-like peptide K-I - frog (Pseudophryne guentheri)

C;Species: Pseudophryne guentheri

C;Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 18-Aug-2000

C;Accession: B60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guentheri.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: B60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

A;Note: this peptide was also found in a deamidated form

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6  
|  
Db 1 Q 1

RESULT 75

C60409

kassinin-like peptide K-II - frog (Pseudophryne guentheri)

C;Species: Pseudophryne guentheri

C;Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 18-Aug-2000

C;Accession: C60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guentheri.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: C60409  
A;Molecule type: protein  
A;Residues: 1-11 <SIM>  
A;Note: this peptide was also found in a deamidated form  
C;Superfamily: unassigned animal peptides  
C;Keywords: amidated carboxyl end; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6  
|  
Db 1 Q 1

Search completed: April 8, 2004, 15:49:24  
Job time : 8.61538 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:47:33 ; Search time 30.3077 Seconds  
(without alignments)  
95.432 Million cell updates/sec

Title: US-09-787-443A-2

Perfect score: 11

Sequence: 1 AKKERQRKDTQ 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1073127 seqs, 262937947 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9223

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : Published\_Applications\_AA:\*

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18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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					Description

1	4	36.4	11	9	US-09-879-936-10	Sequence 10, Appl
2	4	36.4	11	14	US-10-304-443-118	Sequence 118, App
3	3	27.3	11	8	US-08-344-824-44	Sequence 44, Appl
4	3	27.3	11	9	US-09-780-070-37	Sequence 37, Appl
5	3	27.3	11	9	US-09-815-108-9	Sequence 9, Appli
6	3	27.3	11	9	US-09-839-666-12	Sequence 12, Appl
7	3	27.3	11	9	US-09-886-404-13	Sequence 13, Appl
8	3	27.3	11	9	US-09-805-805-8	Sequence 8, Appli
9	3	27.3	11	9	US-09-809-567-16	Sequence 16, Appl
10	3	27.3	11	9	US-09-802-109-1	Sequence 1, Appli
11	3	27.3	11	9	US-09-802-109-2	Sequence 2, Appli
12	3	27.3	11	9	US-09-802-109-3	Sequence 3, Appli
13	3	27.3	11	9	US-09-802-109-4	Sequence 4, Appli
14	3	27.3	11	9	US-09-802-109-5	Sequence 5, Appli
15	3	27.3	11	9	US-09-802-109-6	Sequence 6, Appli
16	3	27.3	11	9	US-09-802-109-8	Sequence 8, Appli
17	3	27.3	11	9	US-09-821-821-24	Sequence 24, Appl
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19	3	27.3	11	9	US-09-873-676-23	Sequence 23, Appl
20	3	27.3	11	9	US-09-891-064A-6	Sequence 6, Appli
21	3	27.3	11	9	US-09-825-414-91	Sequence 91, Appl
22	3	27.3	11	9	US-09-941-611-3	Sequence 3, Appli
23	3	27.3	11	9	US-09-867-274-23	Sequence 23, Appl
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25	3	27.3	11	9	US-09-736-743A-2	Sequence 2, Appli
26	3	27.3	11	9	US-09-984-056-103	Sequence 103, App
27	3	27.3	11	9	US-09-928-175-25	Sequence 25, Appl
28	3	27.3	11	9	US-09-995-542-13	Sequence 13, Appl
29	3	27.3	11	9	US-09-872-832-37	Sequence 37, Appl
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33	3	27.3	11	9	US-09-984-183-4	Sequence 4, Appli
34	3	27.3	11	9	US-09-949-196-15	Sequence 15, Appl
35	3	27.3	11	9	US-09-948-018-22	Sequence 22, Appl
36	3	27.3	11	9	US-09-995-515-14	Sequence 14, Appl
37	3	27.3	11	9	US-09-071-838-204	Sequence 204, App
38	3	27.3	11	9	US-09-895-593-13	Sequence 13, Appl
39	3	27.3	11	9	US-09-896-738-20	Sequence 20, Appl
40	3	27.3	11	9	US-09-981-286A-2	Sequence 2, Appli
41	3	27.3	11	10	US-09-798-051-10	Sequence 10, Appl
42	3	27.3	11	10	US-09-948-193-20	Sequence 20, Appl
43	3	27.3	11	10	US-09-906-393A-9	Sequence 9, Appli
44	3	27.3	11	10	US-09-134-793-2	Sequence 2, Appli
45	3	27.3	11	10	US-09-882-291-43	Sequence 43, Appl
46	3	27.3	11	10	US-09-775-052-2	Sequence 2, Appli
47	3	27.3	11	10	US-09-775-052-16	Sequence 16, Appl
48	3	27.3	11	10	US-09-775-052-52	Sequence 52, Appl
49	3	27.3	11	10	US-09-847-946A-124	Sequence 124, App
50	3	27.3	11	10	US-09-847-946A-125	Sequence 125, App
51	3	27.3	11	10	US-09-876-904A-5	Sequence 5, Appli
52	3	27.3	11	10	US-09-876-904A-10	Sequence 10, Appl
53	3	27.3	11	10	US-09-876-904A-50	Sequence 50, Appl
54	3	27.3	11	10	US-09-876-904A-111	Sequence 111, App
55	3	27.3	11	10	US-09-876-904A-200	Sequence 200, App
56	3	27.3	11	10	US-09-876-904A-232	Sequence 232, App

57	3	27.3	11	10	US-09-876-904A-237	Sequence 237, App
58	3	27.3	11	10	US-09-876-904A-273	Sequence 273, App
59	3	27.3	11	10	US-09-876-904A-354	Sequence 354, App
60	3	27.3	11	10	US-09-876-904A-434	Sequence 434, App
61	3	27.3	11	10	US-09-876-904A-591	Sequence 591, App
62	3	27.3	11	10	US-09-876-904A-597	Sequence 597, App
63	3	27.3	11	10	US-09-820-053A-113	Sequence 113, App
64	3	27.3	11	10	US-09-820-053A-139	Sequence 139, App
65	3	27.3	11	10	US-09-845-612B-20	Sequence 20, Appl
66	3	27.3	11	10	US-09-992-665-55	Sequence 55, Appl
67	3	27.3	11	10	US-09-865-548A-35	Sequence 35, Appl
68	3	27.3	11	10	US-09-997-465B-2	Sequence 2, Appl
69	3	27.3	11	10	US-09-997-465B-18	Sequence 18, Appl
70	3	27.3	11	10	US-09-911-261A-18	Sequence 18, Appl
71	3	27.3	11	10	US-09-798-053-10	Sequence 10, Appl
72	3	27.3	11	10	US-09-854-248-20	Sequence 20, Appl
73	3	27.3	11	10	US-09-962-756-1790	Sequence 1790, Ap
74	3	27.3	11	10	US-09-962-756-2008	Sequence 2008, Ap
75	3	27.3	11	12	US-09-784-553C-50	Sequence 50, Appl
76	3	27.3	11	12	US-09-784-553C-51	Sequence 51, Appl
77	3	27.3	11	12	US-09-784-553C-52	Sequence 52, Appl
78	3	27.3	11	12	US-09-784-553C-53	Sequence 53, Appl
79	3	27.3	11	12	US-09-784-553C-54	Sequence 54, Appl
80	3	27.3	11	12	US-09-784-553C-57	Sequence 57, Appl
81	3	27.3	11	12	US-09-784-553C-60	Sequence 60, Appl
82	3	27.3	11	12	US-10-232-410-11	Sequence 11, Appl
83	3	27.3	11	12	US-10-616-788-16	Sequence 16, Appl
84	3	27.3	11	12	US-09-779-791A-1	Sequence 1, Appl
85	3	27.3	11	12	US-09-822-965-17	Sequence 17, Appl
86	3	27.3	11	12	US-09-822-965-19	Sequence 19, Appl
87	3	27.3	11	12	US-09-823-418-17	Sequence 17, Appl
88	3	27.3	11	12	US-09-823-418-19	Sequence 19, Appl
89	3	27.3	11	12	US-10-622-108-16	Sequence 16, Appl
90	3	27.3	11	13	US-10-007-363-5	Sequence 5, Appl
91	3	27.3	11	14	US-10-139-833-18	Sequence 18, Appl
92	3	27.3	11	14	US-10-083-815-22	Sequence 22, Appl
93	3	27.3	11	14	US-10-108-795-28	Sequence 28, Appl
94	3	27.3	11	14	US-10-108-795-29	Sequence 29, Appl
95	3	27.3	11	14	US-10-142-356-23	Sequence 23, Appl
96	3	27.3	11	14	US-10-156-424A-14	Sequence 14, Appl
97	3	27.3	11	14	US-10-062-710-129	Sequence 129, App
98	3	27.3	11	14	US-10-044-995-3	Sequence 3, Appl
99	3	27.3	11	14	US-10-208-374-2	Sequence 2, Appl
100	3	27.3	11	14	US-10-043-487-538	Sequence 538, App

## ALIGNMENTS

RESULT 1  
 US-09-879-936-10  
 ; Sequence 10, Application US/09879936  
 ; Patent No. US20020045564A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Van Eyk, Jennifer E.  
 ; APPLICANT: Mak, Alan S.  
 ; APPLICANT: Cote, Graham P.

; TITLE OF INVENTION: Methods of Modulating Muscle Contraction  
; FILE REFERENCE: 1997-021-03US  
; CURRENT APPLICATION NUMBER: US/09/879,936  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: 60/050,478  
; PRIOR FILING DATE: 1997-06-23  
; PRIOR APPLICATION NUMBER: 60/089,505  
; PRIOR FILING DATE: 1998-06-16  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(11)  
; OTHER INFORMATION: Residues 423 to 433 of chicken gizzard caldesmon  
; NAME/KEY: PEPTIDE  
; LOCATION: (11)  
; OTHER INFORMATION: Targeted Ser phospho-amino acid  
US-09-879-936-10

Query Match 36.4%; Score 4; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKE 4  
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Db 7 AKKE 10

RESULT 2  
US-10-304-443-118  
; Sequence 118, Application US/10304443  
; Publication No. US20030170229A1  
; GENERAL INFORMATION:  
; APPLICANT: Smithkline Beecham Biologicals s.a.  
; APPLICANT: Peptide Therapeutics Ltd.  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45173CIP  
; CURRENT APPLICATION NUMBER: US/10/304,443  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: US/09/698,906A  
; PRIOR FILING DATE: 2001-02-20  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 118  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human peptide sequence  
US-10-304-443-118

Query Match 36.4%; Score 4; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ERQR 7  
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Db 2 ERQR 5

RESULT 3  
US-08-344-824-44  
; Sequence 44, Application US/08344824  
; Publication No. US20030152580A1  
; GENERAL INFORMATION:  
; APPLICANT: SETTE, Alessandro  
; APPLICANT: SIDNEY, John  
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES  
; NUMBER OF SEQUENCES: 399  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: One Market Plaza, Steuart Street Tower, 20th  
; STREET: Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/344,824  
; FILING DATE: 23-NOV-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/278,634  
; FILING DATE: 21-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bastian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 14137-80-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-344-824-44

Query Match 27.3%; Score 3; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KER 5  
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Db 4 KER 6

RESULT 4  
US-09-780-070-37

; Sequence 37, Application US/09780070  
; Patent No. US20020009752A1  
; GENERAL INFORMATION:  
; APPLICANT: Burke, James  
; APPLICANT: Strittmater, Warren  
; APPLICANT: Nagai, Yoshitaka  
; TITLE OF INVENTION: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE REPEAT DOMAINS  
; TITLE OF INVENTION: AND METHODS OF USE THEREOF  
; FILE REFERENCE: 5405.242  
; CURRENT APPLICATION NUMBER: US/09/780,070  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/189,781  
; PRIOR FILING DATE: 2000-03-16  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 37  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus

US-09-780-070-37

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 5  
US-09-815-108-9

; Sequence 9, Application US/09815108  
; Patent No. US20020009776A1  
; GENERAL INFORMATION:  
; APPLICANT: Saris, Christiaan M.  
; APPLICANT: Sharon, Mu X.  
; APPLICANT: Xia, Min  
; APPLICANT: Boone, Thomas Charles  
; APPLICANT: Covey, Todd  
; TITLE OF INVENTION: Fibroblast Growth Factor Receptor-Like Molecules and  
; TITLE OF INVENTION: Uses Thereof  
; FILE REFERENCE: 99-513-A  
; CURRENT APPLICATION NUMBER: US/09/815,108  
; CURRENT FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: 60/191,379  
; PRIOR FILING DATE: 2000-03-22  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 11  
; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1  
US-09-815-108-9

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
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Db 7 RQR 9

RESULT 6

US-09-839-666-12

; Sequence 12, Application US/09839666  
; Patent No. US20020025513A1  
; GENERAL INFORMATION:  
; APPLICANT: SALLBERG, MATTI  
; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY  
; EXCHANGER  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DARBY & DARBY PC  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/839,666  
; FILING DATE: 19-Apr-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/737,085  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Green, Reza  
; REGISTRATION NUMBER: 38,475  
; REFERENCE/DOCKET NUMBER: 3846/0C569  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-527-7659  
; TELEFAX: 212-753-6237  
; TELEX: 236687  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-839-666-12

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QRK 8  
|||  
Db 1 QRK 3

RESULT 7

US-09-886-404-13

; Sequence 13, Application US/09886404  
; Patent No. US20020037524A1  
; GENERAL INFORMATION:  
; APPLICANT: Medlock, Eugene  
; APPLICANT: Yeh, Richard  
; APPLICANT: Silbiger, Scott M.  
; APPLICANT: Elliot, Gary S.  
; APPLICANT: Nguyen, Hung Q.  
; APPLICANT: Jing, Shuqian  
; TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof  
; FILE REFERENCE: 01017/37128B  
; CURRENT APPLICATION NUMBER: US/09/886,404  
; CURRENT FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 09/810,384  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/266,159  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 60/213,125  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide of HIV  
; OTHER INFORMATION: TAT protein

US-09-886-404-13

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 8

US-09-805-805-8

; Sequence 8, Application US/09805805  
; Patent No. US20020037557A1  
; GENERAL INFORMATION:  
; APPLICANT: Bass, Michael B.

; APPLICANT: Jing, Shuqian  
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Molecules and Uses  
; TITLE OF INVENTION: Thereof  
; FILE REFERENCE: 01-006-A1  
; CURRENT APPLICATION NUMBER: US/09/805,805  
; CURRENT FILING DATE: 2001-03-13  
; PRIOR APPLICATION NUMBER: 60/188,786  
; PRIOR FILING DATE: 2000-03-13  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-805-805-8

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 9

US-09-809-567-16

; Sequence 16, Application US/09809567  
; Patent No. US20020045213A1  
; GENERAL INFORMATION:  
; APPLICANT: Jing, Shuqian  
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof  
; FILE REFERENCE: 01017/36916A  
; CURRENT APPLICATION NUMBER: US/09/809,567  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: 09/724,460  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 60/189,816  
; PRIOR FILING DATE: 2000-03-16  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide  
US-09-809-567-16

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 10  
US-09-802-109-1  
; Sequence 1, Application US/09802109  
; Patent No. US20020058611A1  
; GENERAL INFORMATION:  
; APPLICANT: Stein, Stanley  
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC  
; FILE REFERENCE: 601-1-083  
; CURRENT APPLICATION NUMBER: US/09/802,109  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: 09/044,411  
; PRIOR FILING DATE: 1998-03-19  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; FEATURE:  
; OTHER INFORMATION: Internal sequence from the Tat protein, but with  
; OTHER INFORMATION: an extra Cys not found in natural protein.  
; NAME/KEY: SITE  
; LOCATION: (10)  
; OTHER INFORMATION: Xaa is either Cys(biotin) or Lys(biotin) at this  
; OTHER INFORMATION: position.  
; NAME/KEY: BINDING  
; LOCATION: (10)  
; OTHER INFORMATION: Either Cys(biotin) or Lys(biotin) at this  
; OTHER INFORMATION: position.  
; OTHER INFORMATION: Peptide has an N-terminal carboxylic acid residue.  
; OTHER INFORMATION: Peptide has a C-terminal amide group.  
US-09-802-109-1

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 5 RQR 7

RESULT 11  
US-09-802-109-2  
; Sequence 2, Application US/09802109  
; Patent No. US20020058611A1  
; GENERAL INFORMATION:  
; APPLICANT: Stein, Stanley  
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC  
; FILE REFERENCE: 601-1-083  
; CURRENT APPLICATION NUMBER: US/09/802,109  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: 09/044,411  
; PRIOR FILING DATE: 1998-03-19  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; FEATURE:  
; OTHER INFORMATION: Internal sequence from the Tat protein, but with  
; OTHER INFORMATION: two extra Cys residues not found in the natural  
; OTHER INFORMATION: protein.  
; NAME/KEY: BINDING  
; LOCATION: (10)  
; OTHER INFORMATION: Cys(biotin)  
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.  
; OTHER INFORMATION: Peptide has a C-terminal amide group.  
US-09-802-109-2

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 5 RQR 7

RESULT 12

US-09-802-109-3

; Sequence 3, Application US/09802109  
; Patent No. US20020058611A1  
; GENERAL INFORMATION:  
; APPLICANT: Stein, Stanley  
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC  
; FILE REFERENCE: 601-1-083  
; CURRENT APPLICATION NUMBER: US/09/802,109  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: 09/044,411  
; PRIOR FILING DATE: 1998-03-19  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; FEATURE:  
; OTHER INFORMATION: Internal sequence from the Tat protein, but with  
; OTHER INFORMATION: an extra Lys and an extra Cys not found in the  
; OTHER INFORMATION: natural protein.  
; NAME/KEY: BINDING  
; LOCATION: (10)  
; OTHER INFORMATION: Lys(biotin)  
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.  
; OTHER INFORMATION: Peptide has a C-terminal amide group.  
US-09-802-109-3

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 5 RQR 7

RESULT 13

US-09-802-109-4

; Sequence 4, Application US/09802109  
; Patent No. US20020058611A1  
; GENERAL INFORMATION:  
; APPLICANT: Stein, Stanley  
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC  
; FILE REFERENCE: 601-1-083  
; CURRENT APPLICATION NUMBER: US/09/802,109  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: 09/044,411  
; PRIOR FILING DATE: 1998-03-19  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; FEATURE:  
; OTHER INFORMATION: Internal sequence from the Tat protein, but with  
; OTHER INFORMATION: two extra Cys not found in the natural protein.  
; NAME/KEY: SITE  
; LOCATION: (10)  
; OTHER INFORMATION: Cys is the D isomer at this position.  
; NAME/KEY: BINDING  
; LOCATION: (10)  
; OTHER INFORMATION: D-Cys(biotin)  
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.  
; OTHER INFORMATION: Peptide has a C-terminal amide group.

US-09-802-109-4

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 5 RQR 7

RESULT 14

US-09-802-109-5

; Sequence 5, Application US/09802109  
; Patent No. US20020058611A1  
; GENERAL INFORMATION:  
; APPLICANT: Stein, Stanley  
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC  
; FILE REFERENCE: 601-1-083  
; CURRENT APPLICATION NUMBER: US/09/802,109  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: 09/044,411  
; PRIOR FILING DATE: 1998-03-19

; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; FEATURE:  
; OTHER INFORMATION: Internal sequence from the Tat protein, but with  
; OTHER INFORMATION: an extra Lys and an extra Cys not found in the  
; OTHER INFORMATION: natural protein.  
; NAME/KEY: SITE  
; LOCATION: (10)  
; OTHER INFORMATION: Lys is D isomer at this position.  
; NAME/KEY: BINDING  
; LOCATION: (10)  
; OTHER INFORMATION: D-Lys(biotin)  
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.  
; OTHER INFORMATION: Peptide has a C-terminal amide group.  
US-09-802-109-5

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
      |||  
Db 5 RQR 7

RESULT 15  
US-09-802-109-6  
; Sequence 6, Application US/09802109  
; Patent No. US20020058611A1  
; GENERAL INFORMATION:  
; APPLICANT: Stein, Stanley  
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC  
; FILE REFERENCE: 601-1-083  
; CURRENT APPLICATION NUMBER: US/09/802,109  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: 09/044,411  
; PRIOR FILING DATE: 1998-03-19  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; FEATURE:  
; OTHER INFORMATION: Same as Sequence ID 3, but with a substitution of  
; OTHER INFORMATION: Arg to Gln.  
; NAME/KEY: SITE  
; LOCATION: (10)  
; OTHER INFORMATION: Lys is the D isomer at this position.  
; NAME/KEY: BINDING  
; LOCATION: (10)  
; OTHER INFORMATION: D-Lys(biotin)  
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.

; OTHER INFORMATION: Peptide has a C-terminal amide group.  
US-09-802-109-6

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 5 RQR 7

RESULT 16

US-09-802-109-8

; Sequence 8, Application US/09802109  
; Patent No. US20020058611A1  
; GENERAL INFORMATION:  
; APPLICANT: Stein, Stanley  
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC  
; FILE REFERENCE: 601-1-083  
; CURRENT APPLICATION NUMBER: US/09/802,109  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: 09/044,411  
; PRIOR FILING DATE: 1998-03-19  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; FEATURE:  
; OTHER INFORMATION: All amino acids in this sequence are D amino acid.  
; NAME/KEY: BINDING  
; LOCATION: (2)  
; OTHER INFORMATION: D-Lys(biotin)  
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.  
; OTHER INFORMATION: Peptide has a C-terminal amide group.  
US-09-802-109-8

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 5 RQR 7

RESULT 17

US-09-821-821-24

; Sequence 24, Application US/09821821  
; Patent No. US20020064823A1  
; GENERAL INFORMATION:  
; APPLICANT: Welcher, Andrew A.  
; APPLICANT: Calzone, Frank J.  
; TITLE OF INVENTION: CD20/IgE-Receptor Like Molecules and Uses Thereof  
; FILE REFERENCE: 01017/36938A

; CURRENT APPLICATION NUMBER: US/09/821,821  
; CURRENT FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: US 09/723,258  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: US 60/193,728  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide  
US-09-821-821-24

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 18  
US-09-895-943-13  
; Sequence 13, Application US/09895943  
; Patent No. US20020068323A1  
; GENERAL INFORMATION:  
; APPLICANT: Saris, Chris  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: Thymic Stromal Lymphopoietin Receptor Molecules and  
; TITLE OF INVENTION: Uses Thereof  
; FILE REFERENCE: 00-514-C  
; CURRENT APPLICATION NUMBER: US/09/895,943  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: 60/214,866  
; PRIOR FILING DATE: 2000-06-28  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-895-943-13

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 19

US-09-873-676-23  
; Sequence 23, Application US/09873676  
; Patent No. US20020077289A1  
; GENERAL INFORMATION:  
; APPLICANT: MacDonald, Nicholas J.  
; APPLICANT: Sim, Kim L.  
; TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use  
; FILE REFERENCE: 05213-0378 (43170-259333)  
; CURRENT APPLICATION NUMBER: US/09/873,676  
; CURRENT FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: US 60/209,065  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: US 60/289,387  
; PRIOR FILING DATE: 2001-05-08  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 23  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic binding peptide

US-09-873-676-23

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKD 9  
|||  
Db 5 RKD 7

RESULT 20  
US-09-891-064A-6  
; Sequence 6, Application US/09891064A  
; Patent No. US20020082391A1  
; GENERAL INFORMATION:  
; APPLICANT: James M. Anderson  
; APPLICANT: Christina M. Van Itallie  
; TITLE OF INVENTION: Human Occludin, Its Uses and Enhancement of Drug  
; TITLE OF INVENTION: Absorption Using Occludin Inhibitors  
; FILE REFERENCE: OCR-754.CIP  
; CURRENT APPLICATION NUMBER: US/09/891,064A  
; CURRENT FILING DATE: 2001-06-25  
; PRIOR APPLICATION NUMBER: US 09/142,732  
; PRIOR FILING DATE: 1998-09-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: MS DOS  
; SEQ ID NO 6  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: peptide  
; OTHER INFORMATION: construct used in experiments

US-09-891-064A-6

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKD 9  
|||  
Db 7 RKD 9

RESULT 21

US-09-825-414-91

; Sequence 91, Application US/09825414  
; Patent No. US20020083489A1  
; GENERAL INFORMATION:  
; APPLICANT: Collmer, Alan  
; APPLICANT: Alfano, James R.  
; APPLICANT: Charkowski, Amy O.  
; TITLE OF INVENTION: DNA MOLECULES AND POLYPEPTIDES OF PSEUDOMONAS SYRINGAE  
; TITLE OF INVENTION: HRP PATHOGENICITY ISLAND AND THEIR USES  
; FILE REFERENCE: 19603/3243  
; CURRENT APPLICATION NUMBER: US/09/825,414  
; CURRENT FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/194,160  
; PRIOR FILING DATE: 2000-04-03  
; PRIOR APPLICATION NUMBER: 60/224,604  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/249,548  
; PRIOR FILING DATE: 2000-11-17  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 91  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: human  
; OTHER INFORMATION: immunodeficiency virus TAT protein, transduction  
; OTHER INFORMATION: domain

US-09-825-414-91

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 22

US-09-941-611-3

; Sequence 3, Application US/09941611  
; Patent No. US20020106640A1  
; GENERAL INFORMATION:  
; APPLICANT: DELEYNS, ROBERT J

POLLET, DIRK  
MAERTENS, GEERT  
VAN HEUVERSWUN, HUGO  
TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF  
ANTIBODIES TO HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/941,611  
FILING DATE: 30-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/391,671  
FILING DATE: 1995-02-21  
APPLICATION NUMBER: WO PCT/EP91/02409  
FILING DATE: 13-DEC-1991  
APPLICATION NUMBER: EP 90124241.2  
FILING DATE: 14-DEC-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 7038164000  
TELEFAX: 7038164100  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-941-611-3

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QRK 8  
Db 1 ORK 3

RESULT 23

; Sequence 23, Application US/09867274  
; Patent No. US20020106650A1  
; GENERAL INFORMATION:  
; APPLICANT: Paszty, Christopher  
; APPLICANT: Gao, Yongming  
; TITLE OF INVENTION: Cysteine Knot Polypeptides: Cloaked-2 Molecules and Uses  
Thereof  
; FILE REFERENCE: 01017/37428  
; CURRENT APPLICATION NUMBER: US/09/867,274  
; CURRENT FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: US 60/208,550  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: US 60/223,542  
; PRIOR FILING DATE: 2000-08-04  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 23  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HIV TAT peptide  
US-09-867-274-23

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 24

US-09-955-866-24

; Sequence 24, Application US/09955866  
; Patent No. US20020107363A1  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Michael  
; APPLICANT: Sullivan, John K.  
; APPLICANT: Holst, Paige  
; APPLICANT: Yoshinaga, Steven Kiyoshi  
; TITLE OF INVENTION: B7-Like Polypeptides and Uses Thereof  
; FILE REFERENCE: 00,759-A  
; CURRENT APPLICATION NUMBER: US/09/955,866  
; CURRENT FILING DATE: 2001-09-19  
; PRIOR APPLICATION NUMBER: 60/233,867  
; PRIOR FILING DATE: 2000-09-20  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-955-866-24

Query Match 27.3%; Score 3; DB 9; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 25

US-09-736-743A-2

; Sequence 2, Application US/09736743A  
; Patent No. US20020110869A1  
; GENERAL INFORMATION:  
; APPLICANT: KOVESDI, IMRE  
; APPLICANT: BRUDER, JOSEPH T  
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING CHIMERIC PROTEIN AND RELATED  
VECTOR, CELL AND  
; TITLE OF INVENTION: METHOD OF EXPRESSION  
; FILE REFERENCE: 203591  
; CURRENT APPLICATION NUMBER: US/09/736,743A  
; CURRENT FILING DATE: 2000-12-17  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus

US-09-736-743A-2

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 5 RQR 7

RESULT 26

US-09-984-056-103

; Sequence 103, Application US/09984056  
; Patent No. US20020120106A1  
; GENERAL INFORMATION:  
; APPLICANT: BOGOCH, SAMUEL  
; APPLICANT: BOGOCH, ELENORE S.  
; TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLIKINS AND METHODS OF USE  
; FILE REFERENCE: 09425-46903  
; CURRENT APPLICATION NUMBER: US/09/984,056  
; CURRENT FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: 60/303,396  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: 60/278,761  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: 09/146,755  
; PRIOR FILING DATE: 1998-09-04  
; PRIOR APPLICATION NUMBER: 09/817,144  
; PRIOR FILING DATE: 2001-03-27

; PRIOR APPLICATION NUMBER: 08/198,139  
; PRIOR FILING DATE: 1994-02-17  
; NUMBER OF SEQ ID NOS: 103  
; SOFTWARE: PatentIn 2.1  
; SEQ ID NO 103  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Variola virus  
US-09-984-056-103

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KER 5  
|||  
Db 1 KER 3

RESULT 27

US-09-928-175-25

; Sequence 25, Application US/09928175  
; Patent No. US20020123618A1  
; GENERAL INFORMATION:  
; APPLICANT: Paszty, Christopher J.  
; APPLICANT: Gong, Jianhua  
; APPLICANT: Daugherty, Betsy  
; APPLICANT: Rogers, No. US20020123618Alma  
; TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and  
; TITLE OF INVENTION: Uses Thereof  
; FILE REFERENCE: 00-1229  
; CURRENT APPLICATION NUMBER: US/09/928,175  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/224,455  
; PRIOR FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-928-175-25

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 28

US-09-995-542-13

; Sequence 13, Application US/09995542  
; Patent No. US20020127647A1  
; GENERAL INFORMATION:

; APPLICANT: Shutter, John  
; APPLICANT: Uliaa, Laarni  
; TITLE OF INVENTION: ATP-Binding Cassette Transporter-Like Molecules and  
; TITLE OF INVENTION: Uses Thereof  
; FILE REFERENCE: 00-658-A  
; CURRENT APPLICATION NUMBER: US/09/995,542  
; CURRENT FILING DATE: 2001-11-28  
; PRIOR APPLICATION NUMBER: 60/253,520  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-995-542-13

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 29  
US-09-872-832-37  
; Sequence 37, Application US/09872832  
; Patent No. US20020131960A1  
; GENERAL INFORMATION:  
; APPLICANT: Memorial Sloan-Kettering Cancer Center  
; TITLE OF INVENTION: ARTIFICIAL ANTIGEN PRESENTING CELLS AND METHODS OF USE  
THEREOF  
; FILE REFERENCE: 830002-2003.1  
; CURRENT APPLICATION NUMBER: US/09/872,832  
; CURRENT FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: 60/209,157  
; PRIOR FILING DATE: 2000-02-06  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 37  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-872-832-37

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KER 5  
|||  
Db 4 KER 6

RESULT 30

US-09-927-850-18  
; Sequence 18, Application US/09927850  
; Patent No. US20020137137A1  
; GENERAL INFORMATION:  
; APPLICANT: Welcher, Andrew  
; APPLICANT: Wen, Duanzhi  
; APPLICANT: Kelly, Michael  
; TITLE OF INVENTION: Interferon-Like Molecules and Uses Thereof  
; FILE REFERENCE: 99,372-F  
; CURRENT APPLICATION NUMBER: US/09/927,850  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 09/724,860  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 60/169,720  
; PRIOR FILING DATE: 1999-12-08  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-927-850-18

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 31

US-09-833-079-2  
; Sequence 2, Application US/09833079  
; Patent No. US20020142008A1  
; GENERAL INFORMATION:  
; APPLICANT: O'HANLEY, PETER  
; APPLICANT: DENICH, KENNETH  
; APPLICANT: SCHMIDT, M. ALEXANDER  
; TITLE OF INVENTION: IMMUNOGENIC PILI PRESENTING FOREIGN PEPTIDES, THEIR  
; TITLE OF INVENTION: PRODUCTION AND USE  
; FILE REFERENCE: 050939/0104  
; CURRENT APPLICATION NUMBER: US/09/833,079  
; CURRENT FILING DATE: 2001-04-12  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-833-079-2

Query Match 27.3%; Score 3; DB 9; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 8 AKK 10

RESULT 32

US-09-833-079-17

; Sequence 17, Application US/09833079  
; Patent No. US20020142008A1  
; GENERAL INFORMATION:  
; APPLICANT: O'HANLEY, PETER  
; APPLICANT: DENICH, KENNETH  
; APPLICANT: SCHMIDT, M. ALEXANDER  
; TITLE OF INVENTION: IMMUNOGENIC PILI PRESENTING FOREIGN PEPTIDES, THEIR  
; TITLE OF INVENTION: PRODUCTION AND USE  
; FILE REFERENCE: 050939/0104  
; CURRENT APPLICATION NUMBER: US/09/833,079  
; CURRENT FILING DATE: 2001-04-12  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide

US-09-833-079-17

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 8 AKK 10

RESULT 33

US-09-984-183-4

; Sequence 4, Application US/09984183  
; Patent No. US20020142983A1  
; GENERAL INFORMATION:  
; APPLICANT: AGRAWAL, BABITA  
; APPLICANT: LONGENECKER, MICHAEL B.  
; TITLE OF INVENTION: MUC-1 ANTAGONISTS AND METHODS OF TREATING IMMUNE  
; TITLE OF INVENTION: DISORDERS  
; FILE REFERENCE: 042881/0130  
; CURRENT APPLICATION NUMBER: US/09/984,183  
; CURRENT FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 09/457,354  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 60/111,973  
; PRIOR FILING DATE: 1998-12-11

; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-09-984-183-4

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 34  
US-09-949-196-15  
; Sequence 15, Application US/09949196  
; Patent No. US20020147145A1  
; GENERAL INFORMATION:  
; APPLICANT: Zealand Pharmaceuticals A/S  
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THE DEGRADATION OF  
Cdc25A IN RESPONSE  
; TITLE OF INVENTION: TO DNA DAMAGE  
; FILE REFERENCE: 55888 (45487)  
; CURRENT APPLICATION NUMBER: US/09/949,196  
; CURRENT FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide  
sequence  
US-09-949-196-15

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 35  
US-09-948-018-22  
; Sequence 22, Application US/09948018  
; Patent No. US20020150977A1  
; GENERAL INFORMATION:  
; APPLICANT: Theill et al  
; TITLE OF INVENTION: TNF RECEPTOR-LIKE MOLECULES AND USES THEREOF  
; FILE REFERENCE: 01017/37677

; CURRENT APPLICATION NUMBER: US/09/948,018  
; CURRENT FILING DATE: 2001-09-05  
; PRIOR APPLICATION NUMBER: US 60/230,191  
; PRIOR FILING DATE: 2000-09-05  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 22  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Peptide of HIV TAT protein  
US-09-948-018-22

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 36

US-09-995-515-14

; Sequence 14, Application US/09995515  
; Patent No. US20020151695A1  
; GENERAL INFORMATION:  
; APPLICANT: Jing, Shuqian  
; TITLE OF INVENTION: Transforming Growth Factor-Beta-Related Molecules and  
; TITLE OF INVENTION: Uses Thereof  
; FILE REFERENCE: 00-659-A  
; CURRENT APPLICATION NUMBER: US/09/995,515  
; CURRENT FILING DATE: 2001-11-28  
; PRIOR APPLICATION NUMBER: 60/253,476  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-995-515-14

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 37

US-09-071-838-204

; Sequence 204, Application US/09071838  
; Patent No. US20020152501A1  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, Robert L.

; APPLICANT: Ohad, Nir  
; APPLICANT: Kiyosue, Tomohiro  
; APPLICANT: Yadegari, Ramin  
; APPLICANT: Margossian, Linda  
; APPLICANT: Harada, John  
; APPLICANT: Goldberg, Robert B.  
; TITLE OF INVENTION: Nucleic Acids That Control Seed and  
; TITLE OF INVENTION: Fruit Development in Plants  
; NUMBER OF SEQUENCES: 324  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,838  
; FILING DATE: 01-MAY-1998  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bastian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 023070-086100US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 204:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-071-838-204

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKD 9  
      |||  
Db 3 RKD 5

RESULT 38  
US-09-895-593-13  
; Sequence 13, Application US/09895593  
; Patent No. US20020160949A1  
; GENERAL INFORMATION:  
; APPLICANT: Pandey, Akhilesh  
; APPLICANT: Ozaki, Katsutoshi  
; APPLICANT: Baumann, Heinz

; APPLICANT: Levin, Steven D.  
; APPLICANT: Farr, Andrew G.  
; APPLICANT: Ziegler, Steven F.  
; APPLICANT: Leonard, Warren J.  
; APPLICANT: Lodish, Harvey F.  
; TITLE OF INVENTION: Thymic Stromal Lymphopoietin Receptor Molecules and  
; TITLE OF INVENTION: Uses Thereof  
; FILE REFERENCE: 00-514-E  
; CURRENT APPLICATION NUMBER: US/09/895,593  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: 60/215,658  
; PRIOR FILING DATE: 2000-06-28  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-895-593-13

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 39  
US-09-896-738-20  
; Sequence 20, Application US/09896738  
; Patent No. US20020165347A1  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Michael  
; APPLICANT: Sullivan, John K.  
; APPLICANT: Fang, Mei  
; TITLE OF INVENTION: B7-Like Molecules and Uses Thereof  
; FILE REFERENCE: 00-513-A  
; CURRENT APPLICATION NUMBER: US/09/896,738  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: 60/215,645  
; PRIOR FILING DATE: 2000-06-30  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-896-738-20

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||

Db

7 RQR 9

RESULT 40

US-09-981-286A-2

; Sequence 2, Application US/09981286A  
; Publication No. US20020192799A1  
; GENERAL INFORMATION:  
; APPLICANT: Watowich, Stanley J.  
; APPLICANT: Weaver, Scott C.  
; APPLICANT: Davey, Robert A.  
; TITLE OF INVENTION: Drug Discovery Methods  
; FILE REFERENCE: 265.00260101  
; CURRENT APPLICATION NUMBER: US/09/981,286A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: US 60/240,187  
; PRIOR FILING DATE: 2000-10-13  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cell-permeant polypeptide

US-09-981-286A-2

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 41

US-09-798-051-10

; Sequence 10, Application US/09798051  
; Publication No. US20030008961A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Ke  
; APPLICANT: Cam, Linh  
; APPLICANT: Nakayama, Naoki  
; TITLE OF INVENTION: Chordin-Like-2 Molecules and Uses Thereof  
; FILE REFERENCE: 01-005  
; CURRENT APPLICATION NUMBER: US/09/798,051  
; CURRENT FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1

US-09-798-051-10

Query Match 27.3%; Score 3; DB 10; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 42  
US-09-948-193-20  
; Sequence 20, Application US/09948193  
; Publication No. US20030027335A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruley, H. Earl  
; APPLICANT: Jo, Daewoong  
; TITLE OF INVENTION: Genome Engineering by Cell-Permeable DNA  
; TITLE OF INVENTION: Site-Specific Recombinases  
; FILE REFERENCE: 22000.0109U2  
; CURRENT APPLICATION NUMBER: US/09/948,193  
; CURRENT FILING DATE: 2001-09-07  
; PRIOR APPLICATION NUMBER: 60/230,690  
; PRIOR FILING DATE: 2000-09-07  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human Immunodeficiency Virus  
; FEATURE:  
; OTHER INFORMATION: Description: MTS from HIV Tat  
US-09-948-193-20

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 43  
US-09-906-393A-9  
; Sequence 9, Application US/09906393A  
; Publication No. US20030039970A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Zhou  
; APPLICANT: Xiao, Wuhan  
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED  
; FILE REFERENCE: 1720-1-001CIP  
; CURRENT APPLICATION NUMBER: US/09/906,393A  
; CURRENT FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: 60/218,761  
; PRIOR FILING DATE: 2000-07-17  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9

; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-906-393A-9

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 3 AKK 5

RESULT 44

US-09-134-793-2

; Sequence 2, Application US/09134793  
; Publication No. US20030040038A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; APPLICANT: Jessee, Joel A.  
; TITLE OF INVENTION: INDUCIBLE REGULATORY SYSTEM  
; TITLE OF INVENTION: AND USE THEREOF  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/134,793  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/056,713  
; FILING DATE: 22-AUG-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Corless, Peter F  
; REGISTRATION NUMBER: 33,860  
; REFERENCE/DOCKET NUMBER: 47275  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

; MOLECULE TYPE: protein  
US-09-134-793-2

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 45

US-09-882-291-43

; Sequence 43, Application US/09882291  
; Publication No. US20030040472A1  
; GENERAL INFORMATION:  
; APPLICANT: Zealand Pharmaceuticals A/S  
; TITLE OF INVENTION: No. US20030040472A1 peptide Conjugates  
; FILE REFERENCE: 007-2001  
; CURRENT APPLICATION NUMBER: US/09/882,291  
; CURRENT FILING DATE: 2001-06-15  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 43  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide  
sequence  
US-09-882-291-43

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 46

US-09-775-052-2

; Sequence 2, Application US/09775052  
; Publication No. US20030054000A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/775,052  
; CURRENT FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 09/208,966  
; PRIOR FILING DATE: 1998-12-10  
; PRIOR APPLICATION NUMBER: 60/082,402  
; PRIOR FILING DATE: 1998-04-20  
; PRIOR APPLICATION NUMBER: 60/069,012

; PRIOR FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: human  
US-09-775-052-2

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 47

US-09-775-052-16

; Sequence 16, Application US/09775052  
; Publication No. US20030054000A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/775,052  
; CURRENT FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 09/208,966  
; PRIOR FILING DATE: 1998-12-10  
; PRIOR APPLICATION NUMBER: 60/082,402  
; PRIOR FILING DATE: 1998-04-20  
; PRIOR APPLICATION NUMBER: 60/069,012  
; PRIOR FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: human  
US-09-775-052-16

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 6 RQR 8

RESULT 48

US-09-775-052-52

; Sequence 52, Application US/09775052  
; Publication No. US20030054000A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.

; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/775,052  
; CURRENT FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 09/208,966  
; PRIOR FILING DATE: 1998-12-10  
; PRIOR APPLICATION NUMBER: 60/082,402  
; PRIOR FILING DATE: 1998-04-20  
; PRIOR APPLICATION NUMBER: 60/069,012  
; PRIOR FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 52  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: human  
US-09-775-052-52

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 49  
US-09-847-946A-124  
; Sequence 124, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 124  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:membrane  
; OTHER INFORMATION: translocation domain  
US-09-847-946A-124

Query Match 27.3%; Score 3; DB 10; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 50

US-09-847-946A-125

; Sequence 125, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 125  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:membrane  
; OTHER INFORMATION: translocation domain

US-09-847-946A-125

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 51

US-09-876-904A-5

; Sequence 5, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND  
THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC  
PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fusogenic/NLS peptide  
; OTHER INFORMATION: conjugate from TAT of HIV  
US-09-876-904A-5

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 52  
US-09-876-904A-10  
; Sequence 10, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND  
THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC  
PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic fusogenic  
; OTHER INFORMATION: peptide of TAT  
US-09-876-904A-10

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7

Db            |||  
7 RQR 9

RESULT 53  
US-09-876-904A-50  
; Sequence 50, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND  
THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC  
PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 50  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Human c-myc  
; OTHER INFORMATION: oncprotein  
US-09-876-904A-50

Query Match                    27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity        100.0%; Pred. No. 8.3e+03;  
Matches        3; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

Qy            5 RQR 7  
              |||  
Db            1 RQR 3

RESULT 54  
US-09-876-904A-111  
; Sequence 111, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND  
THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC  
PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 111  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HIV Tat  
protein  
US-09-876-904A-111

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 6 RQR 8

RESULT 55  
US-09-876-904A-200  
; Sequence 200, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND  
THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC  
PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 200  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: *Saccharomyces cerevisiae*  
; FEATURE:  
; OTHER INFORMATION: Karyophilic peptide  
US-09-876-904A-200

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 3 AKK 5

RESULT 56  
US-09-876-904A-232  
; Sequence 232, Application US/09876904A

; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND  
THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC  
PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 232  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Hydrophilic protein  
US-09-876-904A-232

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKD 9  
|||  
Db 8 RKD 10

RESULT 57  
US-09-876-904A-237  
; Sequence 237, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND  
THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC  
PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 237  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Hydrophilic protein  
US-09-876-904A-237

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4  
|||  
Db 7 KKE 9

RESULT 58

US-09-876-904A-273

; Sequence 273, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND  
THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC  
PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 273  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Drosophila sp.  
; FEATURE:  
; OTHER INFORMATION: Recombination repair protein 1

US-09-876-904A-273

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4  
|||  
Db 7 KKE 9

RESULT 59

US-09-876-904A-354

; Sequence 354, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND  
THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC  
PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
; FILE REFERENCE: TB-2002.00

; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 354  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human ATF-3 (in basic region that binds DNA)  
US-09-876-904A-354

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4  
|||  
Db 7 KKE 9

RESULT 60  
US-09-876-904A-434  
; Sequence 434, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND  
THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC  
PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 434  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Drosophila sp.  
; FEATURE:  
; OTHER INFORMATION: Drosophila ultrabiothorax protein (from the  
; OTHER INFORMATION: conserved 61 amino acid homeodomain segment only).  
US-09-876-904A-434

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4  
|||  
Db 8 KKE 10

RESULT 61

US-09-876-904A-591

; Sequence 591, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND  
THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC  
PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 591  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Trout testis H1 (194  
aa).  
US-09-876-904A-591

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 1 AKK 3

RESULT 62

US-09-876-904A-597

; Sequence 597, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND  
THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC  
PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 597

; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Parechinus angulosus  
; FEATURE:  
; OTHER INFORMATION: Sea urchin Parechinus angulosus sperm H1 (248 aa).  
US-09-876-904A-597

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 1 AKK 3

RESULT 63

US-09-820-053A-113

; Sequence 113, Application US/09820053A  
; Publication No. US20030083243A1  
; GENERAL INFORMATION:  
; APPLICANT: Owen, Donald R.  
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES  
; FILE REFERENCE: HELX027  
; CURRENT APPLICATION NUMBER: US/09/820,053A  
; CURRENT FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 165  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 113  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC SEQUENCE  
; NAME/KEY: MOD\_RES  
; LOCATION: (11)  
; OTHER INFORMATION: AMIDATION

US-09-820-053A-113

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
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Db 9 AKK 11

RESULT 64

US-09-820-053A-139

; Sequence 139, Application US/09820053A  
; Publication No. US20030083243A1  
; GENERAL INFORMATION:  
; APPLICANT: Owen, Donald R.  
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES  
; FILE REFERENCE: HELX027  
; CURRENT APPLICATION NUMBER: US/09/820,053A

; CURRENT FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 165  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 139  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC SEQUENCE  
; NAME/KEY: MOD\_RES  
; LOCATION: (11)  
; OTHER INFORMATION: AMIDATION  
US-09-820-053A-139

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3  
|||  
Db 8 AKK 10

RESULT 65  
US-09-845-612B-20  
; Sequence 20, Application US/09845612B  
; Publication No. US20030083261A1  
; GENERAL INFORMATION:  
; APPLICANT: YU, HONGTAO  
; APPLICANT: TANG, ZHANYUN  
; APPLICANT: LUO, XUELIAN  
; APPLICANT: RIZO-REY, JOSE  
; TITLE OF INVENTION: A CLASS OF 12MER PEPTIDES THAT INHIBIT THE FUNCTION OF  
THE MITOTIC CHECK  
; TITLE OF INVENTION: POINT PROTEIN MAD2  
; FILE REFERENCE: UTSD:795  
; CURRENT APPLICATION NUMBER: US/09/845,612B  
; CURRENT FILING DATE: 2001-04-27  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 20  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: HIV-TAT PROTEIN  
US-09-845-612B-20

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 66  
US-09-992-665-55

; Sequence 55, Application US/09992665  
; Publication No. US20030092009A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaia Palm  
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE  
; FILE REFERENCE: CEMINES.002A  
; CURRENT APPLICATION NUMBER: US/09/992,665  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: 60/249,508  
; PRIOR FILING DATE: 2000-11-16  
; NUMBER OF SEQ ID NOS: 380  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 55  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Probe  
US-09-992-665-55

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 8 KDT 10  
|||  
Db 3 KDT 5

RESULT 67  
US-09-865-548A-35  
; Sequence 35, Application US/09865548A  
; Publication No. US20030096298A1  
; GENERAL INFORMATION:  
; APPLICANT: Barnea, Eilon  
; APPLICANT: Beer, Ilan  
; APPLICANT: Ziv, Tamar  
; APPLICANT: Admon, Arie  
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC  
MOLECULES,  
; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES  
; FILE REFERENCE: 01/22080  
; CURRENT APPLICATION NUMBER: US/09/865,548A  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: US 60/290,958  
; PRIOR FILING DATE: 2001-05-16  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 35  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
US-09-865-548A-35

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KER 5  
|||  
Db 4 KER 6

RESULT 68

US-09-997-465B-2

; Sequence 2, Application US/09997465B  
; Publication No. US20030118610A1  
; GENERAL INFORMATION:  
; APPLICANT: Stern, William  
; APPLICANT: Mehta, No. US20030118610Aler M.  
; APPLICANT: Ray, Martha V.L.  
; TITLE OF INVENTION: IMPROVED ORAL DELIVERY OF PEPTIDES USING ENZYME-CLEAVABLE  
MEMBRANE  
; TITLE OF INVENTION: TRANSLOCATORS  
; FILE REFERENCE: P/546-247  
; CURRENT APPLICATION NUMBER: US/09/997,465B  
; CURRENT FILING DATE: 2001-11-29  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-997-465B-2

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 69

US-09-997-465B-18

; Sequence 18, Application US/09997465B  
; Publication No. US20030118610A1  
; GENERAL INFORMATION:  
; APPLICANT: Stern, William  
; APPLICANT: Mehta, No. US20030118610Aler M.  
; APPLICANT: Ray, Martha V.L.  
; TITLE OF INVENTION: IMPROVED ORAL DELIVERY OF PEPTIDES USING ENZYME-CLEAVABLE  
MEMBRANE  
; TITLE OF INVENTION: TRANSLOCATORS  
; FILE REFERENCE: P/546-247  
; CURRENT APPLICATION NUMBER: US/09/997,465B  
; CURRENT FILING DATE: 2001-11-29  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18

; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-997-465B-18

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 70

US-09-911-261A-18

; Sequence 18, Application US/09911261A  
; Publication No. US20030134350A1  
; GENERAL INFORMATION:  
; APPLICANT: Sera, Takashi  
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof  
; FILE REFERENCE: 109845.135  
; CURRENT APPLICATION NUMBER: US/09/911,261A  
; CURRENT FILING DATE: 2001-07-23  
; PRIOR APPLICATION NUMBER: US 60/220,060  
; PRIOR FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 18  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus

US-09-911-261A-18

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 71

US-09-798-053-10

; Sequence 10, Application US/09798053  
; Publication No. US20030158378A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Ke  
; APPLICANT: Cam, Linh  
; APPLICANT: Nakayama, Naoki  
; TITLE OF INVENTION: Chordin-Like-2 Molecules and Uses Thereof  
; FILE REFERENCE: 01-005  
; CURRENT APPLICATION NUMBER: US/09/798,053  
; CURRENT FILING DATE: 2003-03-25  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 10  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-798-053-10

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 RQR 7  
|||  
Db 7 RQR 9

RESULT 72  
US-09-854-248-20  
; Sequence 20, Application US/09854248  
; Publication No. US20030175247A1  
; GENERAL INFORMATION:  
; APPLICANT: Salgaller, Michael L.  
; APPLICANT: Boynton, Alton L.  
; TITLE OF INVENTION: METHOD TO INCREASE CLASS I PRESENTATION OF EXOGENOUS  
; TITLE OF INVENTION: ANTIGENS BY HUMAN DENDRITIC CELLS  
; FILE REFERENCE: 20093-8-1US  
; CURRENT APPLICATION NUMBER: US/09/854,248  
; CURRENT FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: 60/203,758  
; PRIOR FILING DATE: 2000-05-12  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-248-20

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 KKE 4  
|||  
Db 9 KKE 11

RESULT 73  
US-09-962-756-1790  
; Sequence 1790, Application US/09962756  
; Publication No. US20030195147A1  
; GENERAL INFORMATION:  
; APPLICANT: PILLUTLA, RENUKA  
; APPLICANT: BRISSETTE, RENEE  
; APPLICANT: BLUME, ARTHUR J.  
; APPLICANT: SCHAFFER, LAUGE  
; APPLICANT: BRANDT, JAKOB  
; APPLICANT: GOLDSTEIN, NEIL I.

; APPLICANT: SPETZLER, JANE  
; APPLICANT: OSTERGAARD, SOREN  
; APPLICANT: HANSEN, PER HERTZ  
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS  
; FILE REFERENCE: 1878-4051US1  
; CURRENT APPLICATION NUMBER: US/09/962,756  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/538,038  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 09/146,127  
; PRIOR FILING DATE: 1998-09-02  
; NUMBER OF SEQ ID NOS: 2227  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1790  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-962-756-1790

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ERQ 6  
|||  
Db 8 ERQ 10

RESULT 74  
US-09-962-756-2008  
; Sequence 2008, Application US/09962756  
; Publication No. US20030195147A1  
; GENERAL INFORMATION:  
; APPLICANT: PILLUTLA, RENUKA  
; APPLICANT: BRISSETTE, RENEE  
; APPLICANT: BLUME, ARTHUR J.  
; APPLICANT: SCHAFFER, LAUGE  
; APPLICANT: BRANDT, JAKOB  
; APPLICANT: GOLDSTEIN, NEIL I.  
; APPLICANT: SPETZLER, JANE  
; APPLICANT: OSTERGAARD, SOREN  
; APPLICANT: HANSEN, PER HERTZ  
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS  
; FILE REFERENCE: 1878-4051US1  
; CURRENT APPLICATION NUMBER: US/09/962,756  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/538,038  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 09/146,127  
; PRIOR FILING DATE: 1998-09-02  
; NUMBER OF SEQ ID NOS: 2227  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2008  
; LENGTH: 11

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-962-756-2008

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 ERQ 6  
|||  
Db 7 ERQ 9

RESULT 75  
US-09-784-553C-50  
; Sequence 50, Application US/09784553C  
; Publication No. US20040043378A1  
; GENERAL INFORMATION:  
; APPLICANT: ZHOU, MING-MING  
; APPLICANT: AGGARWAL, ANEEL  
; TITLE OF INVENTION: METHODS OF IDENTIFYING MODULATORS OF BROMODOMAINS  
; FILE REFERENCE: 2459-1-003 CIP  
; CURRENT APPLICATION NUMBER: US/09/784,553C  
; CURRENT FILING DATE: 2003-07-08  
; PRIOR APPLICATION NUMBER: 09/510,314  
; PRIOR FILING DATE: 2000-02-22  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 50  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic HIV-1 Tat peptide  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (5)..(5)  
; OTHER INFORMATION: acetylated lysine  
US-09-784-553C-50

Query Match 27.3%; Score 3; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 RQR 7  
|||  
Db 8 RQR 10

Search completed: April 8, 2004, 16:35:33  
Job time : 31.3077 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 27.7692 Seconds  
(without alignments)  
124.984 Million cell updates/sec

Title: US-09-787-443A-2

Perfect score: 11

Sequence: 1 AKKERQRKDQ 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 460

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SPTREMBL\_25:\*

- 1: sp\_archea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rat:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				
No.	Score	Match	Length	DB	ID
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Description

1	4	36.4	11	4	Q9Y3G2	Q9y3g2 homo sapien
2	4	36.4	11	15	Q9DYW4	Q9dyw4 human immun
3	3	27.3	11	4	Q9H4H5	Q9h4h5 homo sapien
4	3	27.3	11	6	Q9TRW5	Q9trw5 bos taurus
5	2	18.2	11	2	Q9R790	Q9r790 borrelia ga
6	2	18.2	11	2	Q9L4F7	Q9l4f7 bacillus ce
7	2	18.2	11	2	Q47606	Q47606 escherichia
8	2	18.2	11	2	Q9R4B1	Q9r4b1 streptococc
9	2	18.2	11	2	Q9S618	Q9s618 prochloroco
10	2	18.2	11	2	Q9R5P3	Q9r5p3 serratia ma
11	2	18.2	11	2	Q9EUZ3	Q9euz3 escherichia
12	2	18.2	11	2	Q8RMI8	Q8rmi8 enterococcu
13	2	18.2	11	2	Q9RBV0	Q9rbv0 pseudomonas
14	2	18.2	11	2	Q9K332	Q9k332 staphylococ
15	2	18.2	11	2	Q9RFZ2	Q9rfz2 mycoplasma
16	2	18.2	11	2	P95518	P95518 pasteurella
17	2	18.2	11	2	Q47420	Q47420 escherichia
18	2	18.2	11	2	Q44090	Q44090 acholeplasm
19	2	18.2	11	2	Q56413	Q56413 escherichia
20	2	18.2	11	2	Q9R446	Q9r446 neisseria g
21	2	18.2	11	2	Q91UY9	Q91uy9 escherichia
22	2	18.2	11	2	Q8GMU3	Q8gmu3 acinetobact
23	2	18.2	11	3	Q9UR95	Q9ur95 pichia angu
24	2	18.2	11	3	Q9HFN8	Q9hfn8 candida rug
25	2	18.2	11	4	Q14759	Q14759 homo sapien
26	2	18.2	11	4	Q16427	Q16427 homo sapien
27	2	18.2	11	4	O60761	O60761 homo sapien
28	2	18.2	11	4	O94785	O94785 homo sapien
29	2	18.2	11	4	Q8NI03	Q8ni03 homo sapien
30	2	18.2	11	5	Q9UAR8	Q9uar8 aedes aegyp
31	2	18.2	11	5	Q9TWX6	Q9twx6 manduca sex
32	2	18.2	11	5	Q99292	Q99292 drosophila
33	2	18.2	11	5	Q8MM58	Q8mm58 heliconius
34	2	18.2	11	5	Q86D32	Q86d32 trypanosoma
35	2	18.2	11	5	Q86D31	Q86d31 trypanosoma
36	2	18.2	11	5	Q95PX6	Q95px6 caenorhabdi
37	2	18.2	11	7	Q9UEX7	Q9uex7 homo sapien
38	2	18.2	11	7	O77911	O77911 oreochromis
39	2	18.2	11	8	Q8MEL7	Q8mel7 sida hooker
40	2	18.2	11	8	Q8MAZ1	Q8maz1 maripa pani
41	2	18.2	11	8	Q8MB39	Q8mb39 wilsonia hu
42	2	18.2	11	8	Q8MEM2	Q8mem2 lagunaria p
43	2	18.2	11	8	Q8MB58	Q8mb58 seddera hir
44	2	18.2	11	8	Q8MAZ3	Q8maz3 maripa repe
45	2	18.2	11	8	Q8MES5	Q8mes5 abelmoschus
46	2	18.2	11	8	Q8MEP0	Q8mep0 hibiscus pe
47	2	18.2	11	8	Q8MES1	Q8mes1 alyogyne pi
48	2	18.2	11	8	Q8MEP3	Q8mep3 hibiscus no
49	2	18.2	11	8	Q8MBE1	Q8mbe1 ipomoea alb
50	2	18.2	11	8	Q8MEQ7	Q8meq7 hibiscus dr
51	2	18.2	11	8	Q35374	Q35374 paramecium
52	2	18.2	11	8	Q8MEL9	Q8mel9 pavonia has
53	2	18.2	11	8	Q8MB77	Q8mb77 odonellia h
54	2	18.2	11	8	Q8MERO	Q8mer0 hibiscus co
55	2	18.2	11	8	Q8MES3	Q8mes3 alyogyne cr
56	2	18.2	11	8	Q8MB79	Q8mb79 aniseia arg
57	2	18.2	11	8	Q8MB97	Q8mb97 merremia pe

58	2	18.2	11	8	Q8MEP5	Q8mep5 hibiscus mi
59	2	18.2	11	8	Q8MER1	Q8mer1 hibiscus ca
60	2	18.2	11	8	Q8MER7	Q8mer7 fioria viti
61	2	18.2	11	9	Q38415	Q38415 bacteriopha
62	2	18.2	11	9	Q37925	Q37925 bacteriopha
63	2	18.2	11	10	Q9S8X4	Q9s8x4 glycine max
64	2	18.2	11	10	Q39784	Q39784 gossypium h
65	2	18.2	11	10	Q82070	Q82070 triticum ae
66	2	18.2	11	10	Q04131	Q04131 lycopersico
67	2	18.2	11	10	P83092	P83092 spinacia ol
68	2	18.2	11	11	P97755	P97755 rattus norv
69	2	18.2	11	11	Q99N81	Q99n81 mus musculu
70	2	18.2	11	11	Q9JLE6	Q9jle6 rattus norv
71	2	18.2	11	11	Q8R2J7	Q8r2j7 mesocricetu
72	2	18.2	11	12	P89269	P89269 xestia c-ni
73	2	18.2	11	12	Q84073	Q84073 influenzae
74	2	18.2	11	12	Q69269	Q69269 equine herp
75	2	18.2	11	13	Q800X7	Q800x7 chelydra se
76	2	18.2	11	13	Q7T285	Q7t285 geochelone
77	2	18.2	11	13	Q7T284	Q7t284 geochelone
78	2	18.2	11	13	Q7T283	Q7t283 geochelone
79	2	18.2	11	13	Q7SX72	Q7sx72 geochelone
80	2	18.2	11	13	Q7SX71	Q7sx71 geochelone
81	2	18.2	11	15	Q9DZ32	Q9dz32 human immun
82	2	18.2	11	16	Q9K7A4	Q9k7a4 bacillus ha
83	1	9.1	11	2	Q9AIY6	Q9aiy6 carsonella
84	1	9.1	11	2	Q68237	Q68237 borrelia bu
85	1	9.1	11	2	Q48933	Q48933 mycobacteri
86	1	9.1	11	2	Q47451	Q47451 escherichia
87	1	9.1	11	2	Q9AIZ7	Q9aiz7 carsonella
88	1	9.1	11	2	Q8RKN1	Q8rkn1 escherichia
89	1	9.1	11	2	Q52526	Q52526 rhizobium s
90	1	9.1	11	2	Q8KHL0	Q8kh10 streptococc
91	1	9.1	11	2	Q47602	Q47602 escherichia
92	1	9.1	11	2	Q8L2T4	Q8l2t4 neisseria m
93	1	9.1	11	2	Q9R7U8	Q9r7u8 pseudomonas
94	1	9.1	11	2	Q9S623	Q9s623 prochloroco
95	1	9.1	11	2	P77404	P77404 escherichia
96	1	9.1	11	2	Q9RQ60	Q9rq60 buchnera ap
97	1	9.1	11	2	P96319	P96319 desulfovibr
98	1	9.1	11	2	Q93RM6	Q93rm6 staphylococ
99	1	9.1	11	2	Q47600	Q47600 escherichia
100	1	9.1	11	2	Q87882	Q87882 mycobacteri

#### ALIGNMENTS

#### RESULT 1

Q9Y3G2

ID Q9Y3G2 PRELIMINARY; PRT; 11 AA.  
 AC Q9Y3G2;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE LSFR2 protein (Fragment).  
 GN LSFR2.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99299247; PubMed=10369878;  
RA Gilley J., Fried M.;  
RT "Extensive gene order differences within regions of conserved synteny  
RT between the Fugu and human genomes: implications for chromosomal  
RT volution and the cloning of disease genes.";  
RL Hum. Mol. Genet. 8:1313-1320(1999).  
DR EMBL; Y17456; CAB44349.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1342 MW; 68C5E5D7A8772324 CRC64;  
  
Query Match 36.4%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQRK 8  
||||  
Db 2 RQRK 5

RESULT 2  
Q9DYW4  
ID Q9DYW4 PRELIMINARY; PRT; 11 AA.  
AC Q9DYW4;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Gag polyprotein (Fragment).  
GN GAG.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20461476; PubMed=11005867;  
RA Martinez-Picado J., DePasquale M.P., Kartsonis N., Hanna G.J.,  
RA Wong J., Finzi D., Rosenberg E., Gunthard H.F., Sutton L., Savara A.,  
RA Petropoulos C.J., Hellmann N., Walker B.D., Richman D.D.,  
RA Siliciano R., D'Aquila R.T.;  
RT "Antiretroviral resistance during successful therapy of HIV type 1  
RT infection.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:10948-10953(2000).  
DR EMBL; AF292846; AAG25476.1; -.  
KW Polyprotein.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1202 MW; 02F874A6240AB2C4 CRC64;  
  
Query Match 36.4%; Score 4; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RKDT 10  
|||  
Db 7 RKDT 10

RESULT 3

Q9H4H5  
ID Q9H4H5 PRELIMINARY; PRT; 11 AA.  
AC Q9H4H5;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE DJ661I20.2 (Novel helicase C-terminal domain and SNF2 N-terminal  
DE domains containing protein) (Fragment).  
GN DJ620E11.1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Skuce C.;  
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AL031669; CAC17164.2; -.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1420 MW; 5EB2C32A3326D053 CRC64;

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 4  
|||  
Db 7 KKE 9

RESULT 4

Q9TRW5  
ID Q9TRW5 PRELIMINARY; PRT; 11 AA.  
AC Q9TRW5;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE 25 kDa protein P25, peptide F4 (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91372400; PubMed=1909972;  
RA Takahashi M., Tomizawa K., Ishiguro K., Sato K., Omori A., Sato S.,  
RA Shiratsuchi A., Uchida T., Imahori K.;  
RT "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a  
RT Ser/Thr-Pro kinase (TPK II) from tau protein kinase fractions.";

RL FEBS Lett. 289:37-43(1991).  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1276 MW; CAF72DAF65A76AA9 CRC64;  
Query Match 27.3%; Score 3; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KER 5  
|||  
Db 1 KER 3

RESULT 5  
Q9R790  
ID Q9R790 PRELIMINARY; PRT; 11 AA.  
AC Q9R790;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Outer surface protein C (Fragment).  
GN OSPC.  
OS *Borrelia garinii*.  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; *Borrelia*.  
OX NCBI\_TaxID=29519;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=G25;  
RX MEDLINE=97426044; PubMed=9282748;  
RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,  
RA Rosa P.;  
RT "the *Borrelia burgdorferi* circular plasmid cp26: conservation of  
RT plasmid structure and targeted inactivation of the *ospC* gene.";  
RL Mol. Microbiol. 25:361-374(1997).  
DR EMBL; U93700; AAC45535.1; -.  
DR GO; GO:0009279; C:external outer membrane (sensu Gram-negativ. . .; IEA.  
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.  
DR GO; GO:0006952; P:defense response; IEA.  
DR InterPro; IPR001800; Lipoprotein\_6.  
DR Pfam; PF01441; Lipoprotein\_6; 1.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1250 MW; 0868D864C5B731A4 CRC64;  
Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3  
||  
Db 2 KK 3

RESULT 6  
Q9L4F7  
ID Q9L4F7 PRELIMINARY; PRT; 11 AA.  
AC Q9L4F7;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE Phosphatidylinositol-specific phospholipase C (PI-PLC)  
DE (Fragment).  
GN PLCA.  
OS Bacillus cereus.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1396;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 14579 type strain;  
RX MEDLINE=20055637; PubMed=10589720;  
RA Okstad O., Gominet M., Purnelle B., Rose M., Lereclus D., Kolsto A.B.;  
RT "Sequence analysis of three *Bacillus cereus* loci under *PICR*-regulated  
RT genes encoding degradative enzymes and enterotoxin.";  
RL Microbiology 145:3129-3138(1999).  
DR EMBL; AJ243711; CAB69804.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1335 MW; 4277A30E20572333 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3  
||  
Db 4 KK 5

RESULT 7  
Q47606  
ID Q47606 PRELIMINARY; PRT; 11 AA.  
AC Q47606;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE REase protein (Fragment).  
GN REASE.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91139577; PubMed=1995588;  
RA Tao T., Bourne J.C., Blumenthal R.M.;  
RT "A family of regulatory genes associated with type II restriction-  
RT modification systems.";  
RL J. Bacteriol. 173:1367-1375(1991).  
DR EMBL; M63622; AAA24562.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1370 MW; 68C1FF9959CB133B CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4  
||  
Db 5 KE 6

RESULT 8

Q9R4B1

ID Q9R4B1 PRELIMINARY; PRT; 11 AA.  
AC Q9R4B1;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE BX protein (Fragment).  
OS Streptococcus pyogenes.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=1314;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95252678; PubMed=7734831;  
RA Gerlach D., Gunther E., Kohler W., Vettermann S., Fleischer B.,  
RA Schmidt K.H.;  
RT "Isolation and characterization of a mitogen characteristic of group A  
RT streptococci (Streptococcus pyogenes).";  
RL Int. J. Med. Microbiol. Virol. Parasitol. Infect. Dis. 282:67-  
RL 82(1995).  
SQ SEQUENCE 11 AA; 1216 MW; CE527287CAA455A2 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TQ 11  
||  
Db 2 TQ 3

RESULT 9

Q9S618

ID Q9S618 PRELIMINARY; PRT; 11 AA.  
AC Q9S618;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Cytochrome b6/f complex subunit IV (Fragment).  
GN PETD.  
OS Prochlorococcus sp.  
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;  
OC Prochlorococcus.  
OX NCBI\_TaxID=1220;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Urbach E., Chisholm S.W.;  
RT "Genetic diversity in Prochlorococcus populations flow cytometrically  
RT sorted from the Sargasso Sea and Gulf Stream.";  
RL Limnol. Oceanog. 43:1615-1630(1998).

DR EMBL; AF070132; AAD20740.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1297 MW; 5CC38013B7633337 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3  
||  
Db 5 KK 6

RESULT 10

Q9R5P3

ID Q9R5P3 PRELIMINARY; PRT; 11 AA.  
AC Q9R5P3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE SM2=NUCLEASE (Fragment).  
OS Serratia marcescens.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Serratia.  
OX NCBI\_TaxID=615;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92134331; PubMed=1663739;  
RA Bannikova G.E., Blagova E.V., Dementiev A.A., Morgunova E.Yu.,  
RA Mikchailov A.M., Shlyapnikov S.V., Varlamov V.P., Vainshtein B.K.;  
RT "Two isoforms of Serratia marcescens nuclease. Crystallization and  
preliminary X-ray investigation of the enzyme.";  
RL Biochem. Int. 24:813-822(1991).  
DR PIR; A27356; A27356.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1179 MW; 6DF18EE04AA045BB CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10  
||  
Db 1 DT 2

RESULT 11

Q9EUVZ3

ID Q9EUVZ3 PRELIMINARY; PRT; 11 AA.  
AC Q9EUVZ3;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE Ribosome binding factor A (Fragment).  
GN RBFA.  
OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IQ490;  
RA Hedegaard J., Kristensen J.E., Nakamura Y., Sperling-Petersen H.U.,  
RA Mortensen K.K.;  
RT "Sequence of the infB gene from Escherichia coli strain IQ489 and  
RT IQ490.";  
RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AJ132862; CAC20133.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1319 MW; 6B234CFE740879CB CRC64;  
  
Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2  
||  
Db 2 AK 3

RESULT 12  
Q8RMI8  
ID Q8RMI8 PRELIMINARY; PRT; 11 AA.  
AC Q8RMI8;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE ErmB (Fragment).  
GN ERMB.  
OS Enterococcus hirae.  
OG Plasmid pMKH1.  
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
OX NCBI\_TaxID=1354;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Borgen K., Sorum M., Wasteson Y., Kruse H., Oppegaard H.;  
RT "Genetic linkage between ermB and vanA in Enterococcus hirae of  
RT poultry origin.";  
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF493942; AAM18554.1; -.  
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
KW Plasmid.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1359 MW; 08A7A8AA49C7273B CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 7 RK 8  
||  
Db 10 RK 11

## RESULT 13

Q9RBV0

ID Q9RBV0 PRELIMINARY; PRT; 11 AA.  
 AC Q9RBV0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Resolvase (Fragment).  
 OS Pseudomonas sp. R9.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=101164;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R9; TRANSPOSON=Tn1404;  
 RX MEDLINE=20011227; PubMed=10543801;  
 RA Schnabel E.L., Jones A.L.;  
 RT "Distribution of tetracycline resistance genes and transposons among  
 RT phylloplane bacteria in Michigan apple orchards.";  
 RL Appl. Environ. Microbiol. 65:4898-4907(1999).  
 DR EMBL; AF157800; AAD48002.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1307 MW; D00B18E258704416 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QR 7  
 ||  
 Db 4 QR 5

## RESULT 14

Q9K332

ID Q9K332 PRELIMINARY; PRT; 11 AA.  
 AC Q9K332;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Geh (Fragment).  
 GN GEH.  
 OS Staphylococcus aureus.  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=1280;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VARIOUS STRAINS;  
 RX MEDLINE=20187516; PubMed=10722640;  
 RA Cramton S.E., Schnell N.F., Gotz F., Bruckner R.;  
 RT "Identification of a new repetitive element in Staphylococcus  
 RT aureus.";  
 RL Infect. Immun. 68:2344-2348(2000).  
 DR EMBL; AF195967; AAF60251.1; -.  
 DR EMBL; AF195963; AAF60243.1; -.  
 DR EMBL; AF195964; AAF60245.1; -.

DR EMBL; AF195965; AAF60247.1; -.  
DR EMBL; AF195966; AAF60249.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1262 MW; 4F978F86AAB1A723 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10  
||  
Db 7 DT 8

RESULT 15

Q9RFZ2  
ID Q9RFZ2 PRELIMINARY; PRT; 11 AA.  
AC Q9RFZ2;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Fructose biphosphate aldolase (Fragment).  
GN FBA.  
OS Mycoplasma mycoides subsp. capri.  
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
OX NCBI\_TaxID=40477;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PG3;  
RX MEDLINE=20193983; PubMed=10727835;  
RA Thiaucourt F., Lorenzon S., David A., Breard A.;  
RT "Phylogeny of the Mycoplasma mycoides cluster as shown by sequencing  
RT of a putative membrane protein gene.";  
RL Vet. Microbiol. 72:251-268(2000).  
DR EMBL; AF162998; AAF15255.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1371 MW; 50B0881A3331FB57 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3  
||  
Db 7 KK 8

RESULT 16

P95518  
ID P95518 PRELIMINARY; PRT; 11 AA.  
AC P95518;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Ribosomal protein RpsA (Fragment).  
GN RPSA.  
OS Pasteurella haemolytica.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellaceae; Mannheimia.  
OX NCBI\_TaxID=75985;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PHL101;  
RX MEDLINE=97164347; PubMed=9011038;  
RA Highlander S.K., Garza O., Brown B.J., Koby S., Oppenheim A.B.;  
RT "Isolation and characterization of the integration host factor genes  
RT of *Pasteurella haemolytica*.";  
RL FEMS Microbiol. Lett. 146:181-188(1997).  
DR EMBL; U56139; AAC44845.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1168 MW; 7A4BFD38D339CDDDB CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2  
||  
Db 8 AK 9

RESULT 17  
Q47420  
ID Q47420 PRELIMINARY; PRT; 11 AA.  
AC Q47420;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE ORF11 protein.  
OS *Escherichia coli*.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; *Escherichia*.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=92041688; PubMed=1657895;  
RA Sharples G.J., Lloyd R.G.;  
RT "Resolution of Holliday junctions in *Escherichia coli*: Identification  
RT of the ruvC gene product as a 19-Kilodalton protein.";  
RL J. Bacteriol. 173:7711-7715(1991).  
DR EMBL; X59551; CAA42127.1; -.  
DR PIR; S19015; S19015.  
SQ SEQUENCE 11 AA; 1215 MW; DD8D6D4D56C6D33D CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2  
||  
Db 4 AK 5

## RESULT 18

Q44090

ID Q44090 PRELIMINARY; PRT; 11 AA.  
 AC Q44090;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Hypothetical export segment (Fragment).  
 OS Acholeplasma laidlawii.  
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;  
 OC Acholeplasmataceae; Acholeplasma.  
 OX NCBI\_TaxID=2148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A-EF22;  
 RA Boyer M.J., Jarhede T.K., Tegman V., Wieslander A.;  
 RT "Sequence regions from Acholeplasma laidlawii which restore export of  
 RT beta-lactamase in Escherichia coli.";  
 RL Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; Z22875; CAA80495.1; -.  
 DR PIR; S33519; S33519.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1234 MW; 5C9D2AE8A682C337 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3  
 ||  
 Db 2 KK 3

## RESULT 19

Q56413

ID Q56413 PRELIMINARY; PRT; 11 AA.  
 AC Q56413;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE IS602L region DNA, 5' end (Fragment).  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TRANSPOSON=Transposon Tn602;  
 RX MEDLINE=87318208; PubMed=2819910;  
 RA Stibitz S., Davies J.E.;  
 RT "Tn602: A naturally occurring relative of Tn903 with direct repeats.";  
 RL Plasmid 17:202-209(1987).  
 DR EMBL; M22735; AAA27464.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1361 MW; 447E8354A05339C3 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2  
||  
Db 1 AK 2

RESULT 20

Q9R446

ID Q9R446 PRELIMINARY; PRT; 11 AA.  
AC Q9R446;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Carbamoyl-phosphate synthase subunit A (Fragment).  
GN CARA.  
OS Neisseria gonorrhoeae.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=485;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MS11, and FA1090;  
RX MEDLINE=95291461; PubMed=7773412;  
RA Lawson F.S., Billowes F.M., Dillon J.A.;  
RT "Organization of carbamoyl-phosphate synthase genes in Neisseria  
gonorrhoeae includes a large, variable intergenic sequence which is  
also present in other Neisseria species.";  
RL Microbiology 141:0-0(0).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MS11, and FA1090;  
RA Brinkman F.S.L., Francis F.M., Dillon J.R.;  
RT "Complexity of the variable sequence between the carbamoyl-phosphate  
synthase genes of Neisseria species.";  
RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF029363; AAC78453.1; -.  
DR EMBL; AF029362; AAC78452.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1178 MW; 0C07A8E3DDD33694 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2  
||  
Db 8 AK 9

RESULT 21

Q91UY9

ID Q91UY9 PRELIMINARY; PRT; 11 AA.  
AC Q91UY9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Insertion site for insertion element IS903.B, upstream of kanamycin  
 DE resistance gene (Fragment).  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TRANSPONSON=Tn2680;  
 RX MEDLINE=85234397; PubMed=2989253;  
 RA Mollet B., Clerget M., Meyer J., Iida S.;  
 RT "Organization of the Tn6-related kanamycin resistance transposon  
 RT Tn2680 carrying two copies of IS26 and an IS903 variant, IS903.B.";  
 RL J. Bacteriol. 163:55-60(1985).  
 DR EMBL; M11420; AAA27427.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1278 MW; 03902598AB0416D0 CRC64;  
  
 Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 6 QR 7  
 ||  
 Db 5 QR 6

RESULT 22  
 Q8GMU3  
 ID Q8GMU3 PRELIMINARY; PRT; 11 AA.  
 AC Q8GMU3;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Putative catalase isozyme (Fragment).  
 GN KATA.  
 OS Acinetobacter lwoffii.  
 OG Plasmid pKLH202.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Moraxellaceae; Acinetobacter.  
 OX NCBI\_TaxID=28090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TC108;  
 RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,  
 RA Nikiforov V.G.;  
 RT "pKLH2-like aberrant transposons and possible mechanisms of their  
 RT dissemination.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AJ250245; CAC80800.1; -.  
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
 KW Plasmid.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1233 MW; 81A15757B333276A CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3  
||  
Db 6 KK 7

RESULT 23

Q9UR95

ID Q9UR95 PRELIMINARY; PRT; 11 AA.  
AC Q9UR95;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Heat shock protein 60 homolog (Fragment).  
OS *Pichia angusta* (Yeast) (*Hansenula polymorpha*).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; *Pichia*.  
OX NCBI\_TaxID=4905;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93223840; PubMed=8096822;  
RA Evers M.E., Huhse B., Titorenko V.I., Kunau W.H., Hartl F.U.,  
RA Harder W., Veenhuis M.;  
RT "Affinity purification of molecular chaperones of the yeast *Hansenula*  
RT polymorpha using immobilized denatured alcohol oxidase.";  
RL FEBS Lett. 321:32-36(1993).  
SQ SEQUENCE 11 AA; 1230 MW; 71872C1779C3372B CRC64;

Query Match 18.2%; Score 2; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4  
||  
Db 3 KE 4

RESULT 24

Q9HFN8

ID Q9HFN8 PRELIMINARY; PRT; 11 AA.  
AC Q9HFN8;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Acyl carrier protein (Fragment).  
GN ACP.  
OS *Candida rugosa* (Yeast) (*Candida cylindracea*).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; mitosporic Saccharomycetales; *Candida*.  
OX NCBI\_TaxID=5481;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Biasio W.;  
RL Thesis (2000), University of Vienna, Austria.

DR EMBL; AJ279021; CAC08812.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1274 MW; D2E4CC3976C40732 CRC64;  
  
Query Match 18.2%; Score 2; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQ 6  
||  
Db 6 RQ 7

RESULT 25

Q14759

ID Q14759 PRELIMINARY; PRT; 11 AA.  
AC Q14759;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Lymphocyte cytosolic protein 2 (Fragment).  
GN LCP2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sunden S.L.F., Carr L.L., Clements J.L., Motto D.G., Koretzky G.A.;  
RT "Polymorphism in and localization of the gene encoding the 76 kDa SH2  
RT domain-containing Leukocyte Protein (SLP-76) to chromosome 5q33.1-  
RT qter.";  
RL Genomics 0:0-0(1995).  
DR EMBL; U44065; AAA93308.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1242 MW; D695104224072DDD CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8  
||  
Db 7 RK 8

RESULT 26

Q16427

ID Q16427 PRELIMINARY; PRT; 11 AA.  
AC Q16427;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)  
DE Dystrophin protein (Fragment).  
GN DYSTROPHIN.  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96163501; PubMed=8566960;  
RA Holder E., Maeda M., Bies R.D.;  
RT "Expression and regulation of the dystrophin Purkinje promoter in  
RT human skeletal muscle, heart, and brain.";  
RL Hum. Genet. 97:232-239(1996).  
DR EMBL; S81419; AAD14362.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1299 MW; DDCC84321AB5A5A2 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ER 5  
||  
Db 8 ER 9

RESULT 27  
O60761  
ID O60761 PRELIMINARY; PRT; 11 AA.  
AC O60761;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE NPT-1 protein (Fragment).  
GN NPT-1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98207718; PubMed=9545579;  
RA Taketani Y., Miyamoto K., Chikamori M., Tanaka K., Yamamoto H.,  
RA Tatsumi S., Morita K., Takeda E.;  
RT "Characterization of the 5' flanking region of the human NPT-1  
RT Na+/phosphate cotransporter gene.";  
RL Biochim. Biophys. Acta 1396:267-272(1998).  
DR EMBL; D83236; BAA25645.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1358 MW; 884E2D4E6734044A CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3  
||  
Db 10 KK 11

RESULT 28

O94785

ID O94785 PRELIMINARY; PRT; 11 AA.  
AC O94785;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)  
DE Thrombopoietin (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sasaki Y., Takahashi T., Nakamura K., Okuno Y., Nakao K.;  
RT "Production of Thrombopoietin by Human Carcinomas and Its Novel mRNA  
RT Isoforms.";  
RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AB014683; BAA34932.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1203 MW; 5FE19F44B6C1A877 CRC64;  
  
Query Match 18.2%; Score 2; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TQ 11  
||  
Db 6 TQ 7

RESULT 29

Q8NI03

ID Q8NI03 PRELIMINARY; PRT; 11 AA.  
AC Q8NI03;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE 25 hydroxyvitamin d3 1-alpha hydroxylase (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ebert R., Schneider D., Jovanovic M., Adamski J., Jakob F.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF500480; AAM21669.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1298 MW; 82C14E84CB533731 CRC64;  
  
Query Match 18.2%; Score 2; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TQ 11  
||

Db

2 TQ 3

RESULT 30

Q9UAR8

ID Q9UAR8 PRELIMINARY; PRT; 11 AA.  
AC Q9UAR8;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Sialokinin I preproprotein (Fragment).  
OS Aedes aegypti (Yellowfever mosquito).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.  
OX NCBI\_TaxID=7159;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Rockefeller/Red; TISSUE=Salivary gland;  
RX MEDLINE=20099025; PubMed=10620041;  
RA Beerntsen B.T., Champagne D.E., Coleman J.L., Campos Y.A., James A.A.;  
RT "Characterization of the Sialokinin I gene encoding the salivary  
RT vasodilator of the yellow fever mosquito, Aedes aegypti.";  
RL Insect Mol. Biol. 8:459-467(1999).  
DR EMBL; AF108100; AAD16884.1; -.  
DR GO; GO:0007268; P:synaptic transmission; IEA.  
DR GO; GO:0007217; P:tachykinin signaling pathway; IEA.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR PROSITE; PS00267; TACHYKININ; 1.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1203 MW; 8BADC77C6B59C33A CRC64;  
  
Query Match 18.2%; Score 2; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

9 DT 10

||

Db

1 DT 2

RESULT 31

Q9TWX6

ID Q9TWX6 PRELIMINARY; PRT; 11 AA.  
AC Q9TWX6;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Juvenile hormone binding protein, JHBP=12.5 kDa CNBR peptide  
DE (Fragment).  
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea;  
OC Sphingidae; Sphinginae; Manduca.  
OX NCBI\_TaxID=7130;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92134256; PubMed=1734862;

RA Touhara K., Prestwich G.D.;  
RT "Binding site mapping of a photoaffinity-labeled juvenile hormone  
RT binding protein.";  
RL Biochem. Biophys. Res. Commun. 182:466-473(1992).  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1071 MW; D232A98E705045BD CRC64;  
  
Query Match 18.2%; Score 2; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 AK 2  
||  
Db 10 AK 11

RESULT 32  
Q99292  
ID Q99292 PRELIMINARY; PRT; 11 AA.  
AC Q99292;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Bicoid protein (Fragment).  
GN BCD.  
OS Drosophila heteroneura (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydriodea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=32382;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91184004; PubMed=2081457;  
RA MacDonald P.M.;  
RT "bicoid mRNA localization signal: phylogenetic conservation of  
RT function and RNA secondary structure.";  
RL Development 110:161-171(1990).  
CC -!-- FUNCTION: BICOID IS SEGMENT-POLARITY PROTEIN THAT PROVIDES  
CC POSITIONAL CUES FOR THE DEVELOPMENT OF HEAD AND THORACIC SEGMENTS.  
CC BCD REGULATES THE EXPRESSION OF ZYGOTIC GENES, POSSIBLY THROUGH  
CC ITS HOMEO DOMAIN, AND INHIBITS THE ACTIVITY OF OTHER MATERNAL GENE  
CC PRODUCTS. IT IS POSSIBLE THAT BCD ALSO BINDS RNA.  
DR EMBL; M32125; AAA28386.1; -.  
DR FlyBase; FBgn0012352; Dhet\bcd.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0003723; F:RNA binding; IEA.  
DR GO; GO:0007275; P:development; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR GO; GO:0007367; P:segment polarity determination; IEA.  
KW DNA-binding; Developmental protein; Homeobox; Nuclear protein;  
KW RNA-binding; Segmentation polarity protein; Transcription regulation.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1221 MW; 8CE802305DD9D6C1 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TQ 11  
||  
Db 4 TQ 5

RESULT 33

Q8MM58

ID Q8MM58 PRELIMINARY; PRT; 11 AA.  
AC Q8MM58;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Mannose phosphate isomerase (Fragment).  
GN MPI.  
OS Heliconius cydno chioneus.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Papilioidea; Nymphalidae; Heliconiinae; Heliconius.  
OX NCBI\_TaxID=171915;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=STRI-B-553-Mpi-1, and STRI-B-553-Mpi-2;  
RA Bull V., Beltran M., Bermingham E., Jiggins C., McMillan O.,  
RA Mallet J.;  
RT "Molecular evidence for gene flow between species of Heliconius.";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF516222; AAM61908.1; -.  
DR EMBL; AF516223; AAM61909.1; -.  
DR GO; GO:0016853; F:isomerase activity; IEA.  
KW Isomerase.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1312 MW; 56A67DB31DD1EAA3 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KD 9  
||  
Db 4 KD 5

RESULT 34

Q86D32

ID Q86D32 PRELIMINARY; PRT; 11 AA.  
AC Q86D32;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Histone H1 (Fragment).  
OS Trypanosoma cruzi.  
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
OX NCBI\_TaxID=5693;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Dm28c;  
RX MEDLINE=22557728; PubMed=12670512;  
RA Sturm N.R., Vargas N.S., Westenberger S.J., Zingales B.,  
RA Campbell D.A.;  
RT "Evidence for multiple hybrid groups in Trypanosoma cruzi.";  
RL Int. J. Parasitol. 33:269-279(2003).  
DR EMBL; AF545075; AAP21903.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1114 MW; CCC1B31E7772CDDD CRC64;  
  
Query Match 18.2%; Score 2; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KK 3  
||  
Db 9 KK 10

RESULT 35  
Q86D31  
ID Q86D31 PRELIMINARY; PRT; 11 AA.  
AC Q86D31;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Histone H1 (Fragment).  
OS Trypanosoma cruzi.  
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
OX NCBI\_TaxID=5693;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sylvio X10;  
RX MEDLINE=22557728; PubMed=12670512;  
RA Sturm N.R., Vargas N.S., Westenberger S.J., Zingales B.,  
RA Campbell D.A.;  
RT "Evidence for multiple hybrid groups in Trypanosoma cruzi.";  
RL Int. J. Parasitol. 33:269-279(2003).  
DR EMBL; AF545076; AAP21906.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1174 MW; CCD1B21E7772CDDD CRC64;  
  
Query Match 18.2%; Score 2; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KK 3  
||  
Db 9 KK 10

RESULT 36  
Q95PX6  
ID Q95PX6 PRELIMINARY; PRT; 11 AA.  
AC Q95PX6;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
GN ZK1236.8.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RA None;  
RT "Genome sequence of the nematode *C. elegans*: a platform for  
investigating biology. The *C. elegans* Sequencing Consortium.";  
RL Science 282:2012-2018(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Favello A.;  
RT "The sequence of *C. elegans* cosmid ZK1236.";  
RL Submitted (MAY-1993) to the EMBL/GenBank/DDBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Waterston R.;  
RT "Direct Submission.";  
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; L13200; AAL11108.1; -.  
DR WormPep; ZK1236.8; CE29629.  
KW Hypothetical protein.  
SQ SEQUENCE 11 AA; 1304 MW; DFA3510A25A76322 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3  
||  
Db 8 KK 9

RESULT 37  
Q9UEX7  
ID Q9UEX7 PRELIMINARY; PRT; 11 AA.  
AC Q9UEX7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Human leucocyte antigen B (Fragment).  
GN HLA-A\*03.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE FROM N.A.  
RA Fae I., Kriks D., Cernava B., Fischer G.F.;  
RT "An novel HLA-A\*03 allele."  
RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AJ252283; CAB65736.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1118 MW; 5191BC69C1A72DD7 CRC64;  
  
Query Match 18.2%; Score 2; DB 7; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TQ 11  
||  
Db 7 TQ 8

RESULT 38  
077911  
ID 077911 PRELIMINARY; PRT; 11 AA.  
AC 077911;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE MHC class II B locus 3 (Fragment).  
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;  
OC Cichlidae; Oreochromis.  
OX NCBI\_TaxID=8128;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98315113; PubMed=9649539;  
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
RA Figueroa F., Sultmann H., Klein J.;  
RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
RT class II B loci.";  
RL Genetics 149:1527-1537(1998).  
DR EMBL; AF050022; AAC41361.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1401 MW; 74342D9002D41B5B CRC64;  
  
Query Match 18.2%; Score 2; DB 7; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ER 5  
||  
Db 8 ER 9

RESULT 39  
Q8MEL7  
ID Q8MEL7 PRELIMINARY; PRT; 11 AA.

AC Q8MEL7;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Sida hookeriana.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Sida.  
OX NCBI\_TaxID=108446;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
RT chloroplast DNA sequences of *ndhF* and the *rpl16* intron.";  
RL Syst. Bot. 27:333-350(2002).  
DR EMBL; AF384624; AAM50396.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;  
  
Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 7 RK 8  
||  
Db 6 RK 7

RESULT 40  
Q8MAZ1  
ID Q8MAZ1 PRELIMINARY; PRT; 11 AA.  
AC Q8MAZ1;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PsbJ (Fragment).  
GN PSBJ.  
OS Maripa paniculata.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC lamiids; Solanales; Convolvulaceae; Maripa.  
OX NCBI\_TaxID=197411;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Stefanovic S., Krueger L., Olmstead R.G.;  
RT "Monophyly of the Convolvulaceae and circumscription of their major  
RT lineages based on DNA sequences of multiple chloroplast loci.";  
RL Am. J. Bot. 0:0-0(2002).  
DR EMBL; AY100937; AAM55869.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10  
||  
Db 3 DT 4

RESULT 41

Q8MB39

ID Q8MB39 PRELIMINARY; PRT; 11 AA.  
AC Q8MB39;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PsbJ (Fragment).  
GN PSBJ.  
OS Wilsonia humilis.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC lamiids; Solanales; Convolvulaceae; Wilsonia.  
OX NCBI\_TaxID=197481;

RN [1]  
RP SEQUENCE FROM N.A.  
RA Stefanovic S., Krueger L., Olmstead R.G.;  
RT "Monophyly of the Convolvulaceae and circumscription of their major  
RT lineages based on DNA sequences of multiple chloroplast loci.";  
RL Am. J. Bot. 0:0-0(2002).  
DR EMBL; AY100914; AAM55777.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10  
||  
Db 3 DT 4

RESULT 42

Q8MEM2

ID Q8MEM2 PRELIMINARY; PRT; 11 AA.  
AC Q8MEM2;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).

GN RPL16.  
 OS *Lagunaria patersonia*.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Lagunaria.  
 OX NCBI\_TaxID=183274;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
 chloroplast DNA sequences of *ndhF* and the *rpl16* intron.";  
 RL Syst. Bot. 27:333-350(2002).  
 DR EMBL; AF384616; AAM50388.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;  
  
 Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 7 RK 8  
 ||  
 Db 6 RK 7

RESULT 43  
 Q8MB58  
 ID Q8MB58 PRELIMINARY; PRT; 11 AA.  
 AC Q8MB58;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE PsbJ (Fragment).  
 GN PSBJ.  
 OS *Seddera hirsuta*.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC lamiids; Solanales; Convolvulaceae; *Seddera*.  
 OX NCBI\_TaxID=197444;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Stefanovic S., Krueger L., Olmstead R.G.;  
 RT "Monophyly of the Convolvulaceae and circumscription of their major  
 RT lineages based on DNA sequences of multiple chloroplast loci.";  
 RL Am. J. Bot. 0:0-0(2002).  
 DR EMBL; AY100905; AAM55743.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10  
||  
Db 3 DT 4

RESULT 44

Q8MAZ3

ID Q8MAZ3 PRELIMINARY; PRT; 11 AA.  
AC Q8MAZ3;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PsbJ (Fragment).  
GN PSBJ.  
OS Maripa repens.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;  
OC lamiids; Solanales; Convolvulaceae; Maripa.  
OX NCBI\_TaxID=197412;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Stefanovic S., Krueger L., Olmstead R.G.;  
RT "Monophyly of the Convolvulaceae and circumscription of their major  
RT lineages based on DNA sequences of multiple chloroplast loci.";  
RL Am. J. Bot. 0:0-0(2002).  
DR EMBL; AY100936; AAM55865.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10  
||  
Db 3 DT 4

RESULT 45

Q8MESS5

ID Q8MESS5 PRELIMINARY; PRT; 11 AA.  
AC Q8MESS5;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Abelmoschus manihot.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;

OC eurosids II; Malvales; Malvaceae; Malvoideae; Abelmoschus.  
OX NCBI\_TaxID=183220;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";  
RL Syst. Bot. 27:333-350(2002).  
DR EMBL; AF384561; AAM50399.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;  
  
Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 7 RK 8  
||  
Db 6 RK 7

RESULT 46  
Q8MEP0  
ID Q8MEP0 PRELIMINARY; PRT; 11 AA.  
AC Q8MEP0;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Hibiscus peralbus.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.  
OX NCBI\_TaxID=183256;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";  
RL Syst. Bot. 27:333-350(2002).  
DR EMBL; AF384598; AAM50370.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;  
  
Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 7 RK 8

||  
Db 6 RK 7

RESULT 47

Q8MES1

ID Q8MES1 PRELIMINARY; PRT; 11 AA.  
AC Q8MES1;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Alyogyne pinoniana.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Alyogyne.  
OX NCBI\_TaxID=183226;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";  
RL Syst. Bot. 27:333-350(2002).  
DR EMBL; AF384566; AAM50404.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;  
  
Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8  
||  
Db 6 RK 7

RESULT 48

Q8MEP3

ID Q8MEP3 PRELIMINARY; PRT; 11 AA.  
AC Q8MEP3;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Hibiscus normanii.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.  
OX NCBI\_TaxID=183253;  
RN [1]

RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
chloroplast DNA sequences of *ndhF* and the *rpl16* intron.";  
RL Syst. Bot. 27:333-350(2002).  
DR EMBL; AF384595; AAM50367.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;  
  
Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8  
||  
Db 6 RK 7

RESULT 49  
Q8MBE1  
ID Q8MBE1 PRELIMINARY; PRT; 11 AA.  
AC Q8MBE1;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PsbJ (Fragment).  
GN PSBJ.  
OS Ipomoea alba.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;  
OC lamiids; Solanales; Convolvulaceae; Ipomoea.  
OX NCBI\_TaxID=89634;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Stefanovic S., Krueger L., Olmstead R.G.;  
RT "Monophyly of the Convolvulaceae and circumscription of their major  
lineages based on DNA sequences of multiple chloroplast loci.";  
RL Am. J. Bot. 0:0-0(2002).  
DR EMBL; AY100861; AAM55568.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 9 DT 10  
||  
Db 3 DT 4

RESULT 50

Q8MEQ7

ID Q8MEQ7 PRELIMINARY; PRT; 11 AA.  
AC Q8MEQ7;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Hibiscus drummondii.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.  
OX NCBI\_TaxID=183239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
RT chloroplast DNA sequences of *ndhF* and the *rpl16* intron.";  
RL Syst. Bot. 27:333-350(2002).  
DR EMBL; AF384581; AAM50353.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8  
||  
Db 6 RK 7

RESULT 51

Q35374

ID Q35374 PRELIMINARY; PRT; 11 AA.  
AC Q35374;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE P1 protein (Fragment).  
OS Paramecium tetraurelia.  
OG Mitochondrion.  
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;  
OC Paramecium.  
OX NCBI\_TaxID=5888;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=stock 172;  
RX MEDLINE=87055241; PubMed=3023187;  
RA Pritchard A.E., Seilhamer J.J., Cummings D.J.;  
RT "Paramecium mitochondrial DNA sequences and RNA transcripts for  
RT cytochrome oxidase subunit I, URF1, and three ORFs adjacent to the

RT replication origin.";  
RL Gene 44:243-253(1986).  
DR EMBL; M15280; AAA79267.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1266 MW; 1D84259D16D046D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QR 7  
||  
Db 7 QR 8

RESULT 52

Q8MEL9  
ID Q8MEL9 PRELIMINARY; PRT; 11 AA.  
AC Q8MEL9;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Pavonia hastata.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Pavonia.  
OX NCBI\_TaxID=183278;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";  
RL Syst. Bot. 27:333-350(2002).  
DR EMBL; AF384622; AAM50394.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8  
||  
Db 6 RK 7

RESULT 53

Q8MB77  
ID Q8MB77 PRELIMINARY; PRT; 11 AA.

AC Q8MB77;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PsbJ (Fragment).  
GN PSBJ.  
OS Odonellia hirtiflora.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC lamiids; Solanales; Convolvulaceae; Odonellia.  
OX NCBI\_TaxID=197424;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Stefanovic S., Krueger L., Olmstead R.G.;  
RT "Monophyly of the Convolvulaceae and circumscription of their major  
RT lineages based on DNA sequences of multiple chloroplast loci.";  
RL Am. J. Bot. 0:0-0(2002).  
DR EMBL; AY100897; AAM55711.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10  
||  
Db 3 DT 4

RESULT 54  
Q8MERO  
ID Q8MERO PRELIMINARY; PRT; 11 AA.  
AC Q8MERO;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Hibiscus coatesii.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.  
OX NCBI\_TaxID=183236;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";  
RL Syst. Bot. 27:333-350(2002).  
DR EMBL; AF384578; AAM50416.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.

FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;  
Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8  
||  
Db 6 RK 7

RESULT 55

Q8MES3

ID Q8MES3 PRELIMINARY; PRT; 11 AA.  
AC Q8MES3;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Alyogyne cravenii.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Alyogyne.  
OX NCBI\_TaxID=183223;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";  
RL Syst. Bot. 27:333-350(2002).  
DR EMBL; AF384563; AAM50401.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8  
||  
Db 6 RK 7

RESULT 56

Q8MB79

ID Q8MB79 PRELIMINARY; PRT; 11 AA.  
AC Q8MB79;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE PsbJ (Fragment).  
 GN PSBJ.  
 OS *Aniseia argentina*.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;  
 OC lamiids; Solanales; Convolvulaceae; *Aniseia*.  
 OX NCBI\_TaxID=197349;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Stefanovic S., Krueger L., Olmstead R.G.;  
 RT "Monophyly of the Convolvulaceae and circumscription of their major  
 RT lineages based on DNA sequences of multiple chloroplast loci.";  
 RL Am. J. Bot. 0:0-0(2002).  
 DR EMBL; AY100895; AAM55703.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;  
  
 Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 9 DT 10  
 ||  
 Db 3 DT 4

RESULT 57  
 Q8MB97  
 ID Q8MB97 PRELIMINARY; PRT; 11 AA.  
 AC Q8MB97;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE PsbJ (Fragment).  
 GN PSBJ.  
 OS *Merremia peltata*.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;  
 OC lamiids; Solanales; Convolvulaceae; *Merremia*.  
 OX NCBI\_TaxID=197416;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Stefanovic S., Krueger L., Olmstead R.G.;  
 RT "Monophyly of the Convolvulaceae and circumscription of their major  
 RT lineages based on DNA sequences of multiple chloroplast loci.";  
 RL Am. J. Bot. 0:0-0(2002).  
 DR EMBL; AY100885; AAM55663.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10  
||  
Db 3 DT 4

RESULT 58

Q8MEP5

ID Q8MEP5 PRELIMINARY; PRT; 11 AA.  
AC Q8MEP5;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Hibiscus microchlaenus.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.  
OX NCBI\_TaxID=183251;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
chloroplast DNA sequences of ndhF and the rpl16 intron.";  
RL Syst. Bot. 27:333-350(2002).  
DR EMBL; AF384593; AAM50365.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8  
||  
Db 6 RK 7

RESULT 59

Q8MER1

ID Q8MER1 PRELIMINARY; PRT; 11 AA.  
AC Q8MER1;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Hibiscus calyphyllus.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.  
OX NCBI\_TaxID=183235;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";  
RL Syst. Bot. 27:333-350(2002).  
DR EMBL; AF384577; AAM50415.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;  
Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8  
||  
Db 6 RK 7

RESULT 60  
Q8MER7  
ID Q8MER7 PRELIMINARY; PRT; 11 AA.  
AC Q8MER7;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Fioria vitifolia.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Fioria.  
OX NCBI\_TaxID=183231;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";  
RL Syst. Bot. 27:333-350(2002).  
DR EMBL; AF384570; AAM50408.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;  
Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8  
||  
Db 6 RK 7

RESULT 61  
Q38415  
ID Q38415 PRELIMINARY; PRT; 11 AA.  
AC Q38415;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Ant1 protein (Fragment).  
OS Bacteriophage P7.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;  
OC P1-like viruses.  
OX NCBI\_TaxID=10682;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90335968; PubMed=1696181;  
RA Citron M., Schuster H.;  
RT "The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.";  
RL Cell 62:591-598(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92319637; PubMed=1620606;  
RA Citron M., Schuster H.;  
RT "The c4 repressor of bacteriophage P1 is a processed 77 base antisense  
RT RNA.";  
RL Nucleic Acids Res. 20:3085-3090(1992).  
DR EMBL; M35139; AAA32437.1; -.  
DR PIR; S42449; S42449.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1315 MW; 38A55C6D11B2C737 CRC64;

Query Match 18.2%; Score 2; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3  
||  
Db 2 KK 3

RESULT 62  
Q37925  
ID Q37925 PRELIMINARY; PRT; 11 AA.  
AC Q37925;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Bacteriophage fr replicase (Fragment).  
OS Bacteriophage fr.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;  
OC Levivirus.  
OX NCBI\_TaxID=12017;  
RN [1]

RP SEQUENCE FROM N.A.  
RA Berzin V.M., Gribanov V.A., Cielens I.E., Jansone I.V., Gren E.J.;  
RT "The nucleotide sequence of the regulatory region of phage fr  
replicase cistron.";  
RL Bioorg. Khim. 7:306-308(1981).  
DR EMBL; M34834; AAA32193.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1285 MW; 8BD43470C33321B1 CRC64;  
  
Query Match 18.2%; Score 2; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3  
||  
Db 6 KK 7

RESULT 63  
Q9S8X4  
ID Q9S8X4 PRELIMINARY; PRT; 11 AA.  
AC Q9S8X4;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Vegetative storage protein 94 peptide 3, VSP94=LIPOXYGENASE  
(Fragment).  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92361246; PubMed=1822994;  
RA Tranbarger T.J., Franceschi V.R., Hildebrand D.F., Grimes H.D.;  
RT "The soybean 94-kilodalton vegetative storage protein is a  
RT lipoxygenase that is localized in paraveinal mesophyll cell  
RT vacuoles.";  
RL Plant Cell 3:973-987(1991).  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1366 MW; 9B337C3C0DD9CB1A CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 4 ER 5  
||  
Db 9 ER 10

RESULT 64  
Q39784  
ID Q39784 PRELIMINARY; PRT; 11 AA.  
AC Q39784;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)  
DE Alcohol dehydrogenase 2b-2 (Fragment).  
OS *Gossypium hirsutum* (Upland cotton).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; *Gossypium*.  
OX NCBI\_TaxID=3635;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Blue Tag Siokra;  
RA Millar A.A., Dennis E.S.;  
RL Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; U53705; AAA98988.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1161 MW; D67F443942D6D87D CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2  
||  
Db 10 AK 11

RESULT 65  
082070  
ID 082070 PRELIMINARY; PRT; 11 AA.  
AC 082070;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE RNA polymerase (EC 2.7.7.6) (Fragment).  
OS *Triticum aestivum* (Wheat).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; *Triticum*.  
OX NCBI\_TaxID=4565;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Chinese Spring;  
RA Young D.A., Allen R., Harvey A.J., Lonsdale D.M.;  
RT "Characterization of a gene encoding a single-subunit RNA polymerase  
from maize which is alternatively spliced.";  
RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AJ005344; CAA06489.1; -.  
DR GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.  
DR GO; GO:0003900; F:DNA-directed RNA polymerase I activity; IEA.  
DR GO; GO:0003901; F:DNA-directed RNA polymerase II activity; IEA.  
DR GO; GO:0003902; F:DNA-directed RNA polymerase III activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
KW Nucleotidyltransferase; Transferase.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1329 MW; CD96344923240AB2 CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8  
||  
Db 6 RK 7

RESULT 66

Q04131

ID Q04131 PRELIMINARY; PRT; 11 AA.  
AC Q04131;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Wound induced protein (Fragment).  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;  
OC lamiids; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4081;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=pik-red; TISSUE=Pericarp;  
RX MEDLINE=91355936; PubMed=1715787;  
RA Parsons B.L., Mattoo A.K.;  
RT "Wound regulated accumulation of specific transcripts in tomato fruit:  
RT interactions with fruit development, ethylene and light.";  
RL Plant Mol. Biol. 17:453-464(1991).  
DR EMBL; X59884; CAA42539.1; -.  
DR PIR; S19775; S19775.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1278 MW; 92CB257828733325 CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3  
||  
Db 5 KK 6

RESULT 67

P83092

ID P83092 PRELIMINARY; PRT; 11 AA.  
AC P83092;  
DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE 33.6 kDa protein (Fragment).  
OS Spinacia oleracea (Spinach).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;  
OC Caryophyllales; Amaranthaceae; Spinacia.

OX NCBI\_TaxID=3562;  
RN [1]  
RP SEQUENCE, AND SUBCELLULAR LOCATION.  
RA Schubert M., Peterson U., Funk C., Schroeder W.P., Kieselbach T.;  
RL Submitted (AUG-2001) to Swiss-Prot.  
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST; WITHIN THE THYLAKOID LUMEN.  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1274 MW; 95344C4D21AAB775 CRC64;  
Query Match 18.2%; Score 2; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10  
||  
Db 6 DT 7

RESULT 68  
P97755  
ID P97755 PRELIMINARY; PRT; 11 AA.  
AC P97755;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)  
DE Secretogranin II (SGII) (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96343805; PubMed=8756552;  
RA Jones L.C., Day R.N., Pittler S.J., Valentine D.L., Scammell J.G.;  
RT "Cell-specific expression of the rat secretogranin II promoter.";  
RL Endocrinology 137:3815-3822(1996).  
DR EMBL; AF107301; -; NOT\_ANNOTATED\_CDS.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1298 MW; 3E4E8DA446C1B5A7 CRC64;

Query Match 18.2%; Score 2; DB 11; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 10 TQ 11  
||  
Db 6 TQ 7

RESULT 69  
Q99N81  
ID Q99N81 PRELIMINARY; PRT; 11 AA.  
AC Q99N81;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Delta like 1 (Fragment).  
GN DLL1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Nakayama K.;  
RT "Multiple POU-binding motifs, recognized by tissue-specific nuclear  
RT factor(S), are important for Dll1 gene expression in developing neural  
RT precursor cells.";  
RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AB050457; BAB43867.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1259 MW; 33C3634CBDC40B07 CRC64;  
  
Query Match 18.2%; Score 2; DB 11; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 4 ER 5  
||  
Db 5 ER 6  
  
RESULT 70  
Q9JLE6  
ID Q9JLE6 PRELIMINARY; PRT; 11 AA.  
AC Q9JLE6;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE Thioredoxin reductase (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Rundlof A.-K., Arner E.S.J.;  
RT "Genomic sequence of parts of the rat thioredoxin reductase 1 gene.";  
RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF189711; AAF26304.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1255 MW; 804D1A1E6DDAA325 CRC64;  
  
Query Match 18.2%; Score 2; DB 11; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 8 KD 9  
||  
Db 5 KD 6

## RESULT 71

Q8R2J7

ID Q8R2J7 PRELIMINARY; PRT; 11 AA.  
 AC Q8R2J7;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Microphthalmia-associated transcription factor (Fragment).  
 GN MITF.  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Graw J., Pretsch W., Loester I.;  
 RT "Mutation in intron 6 of the hamster mitf gene leads to skipping of  
 the subsequent exon and creates a dominant animal model for the human  
 RT Waardenburg syndrome type II.";  
 RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AJ458439; CAD30263.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1532 MW; 69D76B515449D414 CRC64;  
  
 Query Match 18.2%; Score 2; DB 11; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 4 ER 5  
 ||  
 Db 1 ER 2

## RESULT 72

P89269

ID P89269 PRELIMINARY; PRT; 11 AA.  
 AC P89269;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE DNA binding protein homolog (Fragment).  
 OS Xestia c-nigrum granulosis virus (XnGV) (Xestia c-nigrum  
 OS granulovirus).  
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.  
 OX NCBI\_TaxID=51677;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=alpha-4;  
 RX MEDLINE=98271593; PubMed=9608666;  
 RA Goto C., Hayakawa T., Maeda S.;  
 RT "Genome organization of Xestia c-nigrum granulovirus.";  
 RL Virus Genes 16:199-210(1998).  
 DR EMBL; U70897; AAB46487.1; -.  
 FT NON\_TER 1 1

SQ SEQUENCE 11 AA; 1371 MW; 6F05444F52C1E454 CRC64;  
Query Match 18.2%; Score 2; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QR 7  
||  
Db 2 QR 3

RESULT 73

Q84073

ID Q84073 PRELIMINARY; PRT; 11 AA.  
AC Q84073;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Influenza A/fpv/rostock/34 (H7n1), polymerase 3 (Seg 3), 3' end of  
DE vrna (Initiator region for protein coding) (Fragment).  
OS Influenzavirus A.  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza A viruses.  
OX NCBI\_TaxID=197911;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=80034428; PubMed=493121;  
RA Robertson J.S.;  
RT "5' and 3' terminal nucleotide sequences of the rna genome segments of  
RT influenza virus.";  
RL Nucleic Acids Res. 6:3745-3757(1979).  
DR EMBL; J02123; AAA43612.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1400 MW; CC2007F7A6C412C9 CRC64;

Query Match 18.2%; Score 2; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RQ 6  
||  
Db 6 RQ 7

RESULT 74

Q69269

ID Q69269 PRELIMINARY; PRT; 11 AA.  
AC Q69269;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein (Fragment).  
GN IE.  
OS Equine herpesvirus 1.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Varicellovirus.  
OX NCBI\_TaxID=10326;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Kentucky A;  
 RX MEDLINE=90064773; PubMed=2555546;  
 RA Harty R.N., Colle C.F., Grundy F.J., O'Callaghan D.J.;  
 RT "Mapping the termini and intron of the spliced immediate-early  
 RT transcript of equine herpesvirus 1.";  
 RL J. Virol. 63:5101-5110(1989).  
 DR EMBL; M30497; AAA66553.1; -.  
 KW Hypothetical protein.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1224 MW; D93837E0CAB5A416 CRC64;  
  
 Query Match 18.2%; Score 2; DB 12; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 6 QR 7  
 ||  
 Db 4 QR 5  
  
 RESULT 75  
 Q800X7  
 ID Q800X7 PRELIMINARY; PRT; 11 AA.  
 AC Q800X7;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Vacuolar H-ATPase B subunit (Fragment).  
 OS Chelydra serpentina serpentina (common snapping turtle).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.  
 OX NCBI\_TaxID=134619;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21876906; PubMed=11882478;  
 RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;  
 RT "Octylphenol (OP) alters the expression of members of the amyloid  
 RT protein family in the hypothalamus of the snapping turtle, Chelydra  
 RT serpentina serpentina.";  
 RL Environ. Health Perspect. 110:269-275(2002).  
 DR EMBL; AF469184; AAO48730.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA; 1350 MW; 2FC8B6D0B5BAB417 CRC64;  
  
 Query Match 18.2%; Score 2; DB 13; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 AK 2  
 ||  
 Db 9 AK 10

Search completed: April 8, 2004, 15:46:01  
 Job time : 28.7692 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 5.15385 Seconds  
(without alignments)  
111.135 Million cell updates/sec

Title: US-09-787-443A-2

Perfect score: 11

Sequence: 1 AKKERQRKDTQ 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 70

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	2	18.2	11	1	ASL2_BACSE	P83147 bacteroides
2	2	18.2	11	1	BRK_MEGFL	P12797 megascolia
3	2	18.2	11	1	NXSN_PSETE	P59072 pseudonaja
4	2	18.2	11	1	PKC1_CARMO	P82684 carausius m
5	2	18.2	11	1	PQQC_PSEFL	P55173 pseudomonas
6	2	18.2	11	1	Q2OA_COMTE	P80464 comamonas t
7	2	18.2	11	1	TKNA_RANRI	P29207 rana ridibu
8	2	18.2	11	1	TKND_RANCA	P22691 rana catesb
9	2	18.2	11	1	TKN_ELEMO	P01293 eledone mos
10	2	18.2	11	1	UXB2_YEAST	P99013 saccharomyc
11	1	9.1	11	1	ANGT_CRIGE	P09037 crinia geor
12	1	9.1	11	1	ASL1_BACSE	P83146 bacteroides
13	1	9.1	11	1	BPP3_BOTIN	P30423 bothrops in
14	1	9.1	11	1	BPP4_BOTIN	P30424 bothrops in
15	1	9.1	11	1	BPPB_AGKHA	P01021 agkistrodon
16	1	9.1	11	1	BPP_AGKHP	P04562 agkistrodon
17	1	9.1	11	1	CA21_LITCI	P82087 litoria cit

18	1	9.1	11	1	CA22_LITCI	P82088 litoria cit
19	1	9.1	11	1	CA31_LITCI	P82089 litoria cit
20	1	9.1	11	1	CA32_LITCI	P82090 litoria cit
21	1	9.1	11	1	CA41_LITCI	P82091 litoria cit
22	1	9.1	11	1	CA42_LITCI	P82092 litoria cit
23	1	9.1	11	1	CEP1_ACHFU	P22790 achatina fu
24	1	9.1	11	1	CORZ_PERAM	P11496 periplaneta
25	1	9.1	11	1	COXA_CANFA	P99501 canis famil
26	1	9.1	11	1	CSI5_BACSU	P81095 bacillus su
27	1	9.1	11	1	CX5A_CONAL	P58848 conus aulic
28	1	9.1	11	1	CX5B_CONAL	P58849 conus aulic
29	1	9.1	11	1	CXL1_CONMR	P58807 conus marmo
30	1	9.1	11	1	EFG_CLOPA	P81350 clostridium
31	1	9.1	11	1	ES1_RAT	P56571 rattus norv
32	1	9.1	11	1	FAR6_PENMO	P83321 penaeus mon
33	1	9.1	11	1	FAR9_CALVO	P41864 calliphora
34	1	9.1	11	1	HS70_PINPS	P81672 pinus pinas
35	1	9.1	11	1	LADD_ONCMY	P81018 oncorhynchus
36	1	9.1	11	1	LPW_THETH	P05624 thermus the
37	1	9.1	11	1	LSK1_LEUMA	P04428 leucophaea
38	1	9.1	11	1	LSKP_PERAM	P36885 periplaneta
39	1	9.1	11	1	MHBI_KLEPN	P80580 klebsiella
40	1	9.1	11	1	MLG_THETS	P41989 theromyzon
41	1	9.1	11	1	MORN_HUMAN	P01163 homo sapien
42	1	9.1	11	1	NUHM_CANFA	P49820 canis famil
43	1	9.1	11	1	OAIF_SARBU	P83518 sarcophaga
44	1	9.1	11	1	PVK1_PERAM	P41837 periplaneta
45	1	9.1	11	1	RANC_RANPI	P08951 rana pipien
46	1	9.1	11	1	RE41_LITRU	P82074 litoria rub
47	1	9.1	11	1	RR2_CONAM	P42341 conopholis
48	1	9.1	11	1	RRPL_CHAV	P13179 chandipura
49	1	9.1	11	1	RS30_ONCMY	P83328 oncorhynchus
50	1	9.1	11	1	T2P1_PROVU	P31031 proteus vul
51	1	9.1	11	1	TIN1_HOPTI	P82651 hoplobatrac
52	1	9.1	11	1	TIN4_HOPTI	P82654 hoplobatrac
53	1	9.1	11	1	TKC2_CALVO	P41518 calliphora
54	1	9.1	11	1	TKN1_PSEGU	P42986 pseudophryne
55	1	9.1	11	1	TKN1_UPEIN	P82026 uperoleia i
56	1	9.1	11	1	TKN1_UPERU	P08612 uperoleia r
57	1	9.1	11	1	TKN2_PSEGU	P42987 pseudophryne
58	1	9.1	11	1	TKN2_UPERU	P08616 uperoleia r
59	1	9.1	11	1	TKN3_PSEGU	P42988 pseudophryne
60	1	9.1	11	1	TKN4_PSEGU	P42989 pseudophryne
61	1	9.1	11	1	TKN5_PSEGU	P42990 pseudophryne
62	1	9.1	11	1	TKNA_CHICK	P19850 gallus gallus
63	1	9.1	11	1	TKNA_GADMO	P28498 gadus morhua
64	1	9.1	11	1	TKNA_HORSE	P01290 equus caballus
65	1	9.1	11	1	TKNA_ONCMY	P28499 oncorhynchus
66	1	9.1	11	1	TKNA_RANCA	P22688 rana catesbeiana
67	1	9.1	11	1	TKNA_SCYCA	P41333 scyliorhinus
68	1	9.1	11	1	TKN_PHYFU	P08615 physalaemus
69	1	9.1	11	1	UF05_MOUSE	P38643 mus musculus
70	1	9.1	11	1	ULAG_HUMAN	P31933 homo sapiens

#### ALIGNMENTS

RESULT 1

ASL2\_BACSE

ID ASL2\_BACSE STANDARD; PRT; 11 AA.

AC P83147;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Acharan sulfate lyase 2 (EC 4.2.2.-) (Fragment).

OS Bacteroides stercoris.

OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;

OC Bacteroidaceae; Bacteroides.

OX NCBI\_TaxID=46506;

RN [1]

RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.

RC STRAIN=HJ-15;

RX MEDLINE=21223019; PubMed=11322884;

RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;

RT "Purification and characterization of acharan sulfate lyases, two novel heparinases, from Bacteroides stercoris HJ-15.";

RL Eur. J. Biochem. 268:2635-2641(2001).

CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent, heparin and heparan sulfate.

CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and lead. Activated by reducing agents, such as DL-dithiothreitol and 2-mercaptopethanol.

CC -!- SUBUNIT: Monomer.

CC -!- PTM: The N-terminus is blocked.

CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is 7.2 and optimum temperature 45 degrees Celsius.

KW Lyase; Heparin-binding.

FT NON\_TER 1 1

FT NON\_TER 11 11

SQ SEQUENCE 11 AA; 1195 MW; D79D897C7AA451AD CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QR 7

||

Db 10 QR 11

RESULT 2

BRK\_MEGFL

ID BRK\_MEGFL STANDARD; PRT; 11 AA.

AC P12797;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Megascoliakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like peptide ([Thr6]bradykinin)].

OS Megascolia flavifrons (Garden dagger wasp) (Solitary wasp).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;

OC Scoliidae; Megascolia.

OX NCBI\_TaxID=7437;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=87293024; PubMed=3617088;  
 RA Yasuhara T., Mantel P., Nakajima T., Piek T.;  
 RT "Two kinins isolated from an extract of the venom reservoirs of the  
 RT solitary wasp *Megascolia flavifrons*.";  
 RL Toxicon 25:527-535(1987).  
 RN [2]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RA Nakajima T., Piek T., Yasuhara T., Mantel P.;  
 RT "Two kinins isolated from the venom of *Megascolia flavifrons*.";  
 RL Toxicon 26:34-34(1988).  
 CC -!- FUNCTION: Both proteins have bradykinin-like, although lower  
 CC activities (e.g. smooth muscle contraction).  
 CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.  
 CC -!- SIMILARITY: Belongs to the bradykinin family.  
 DR PIR; B26744; B26744.  
 DR GO; GO:0005615; C:extracellular space; IDA.  
 DR GO; GO:0045776; P:negative regulation of blood pressure; ISS.  
 DR GO; GO:0045987; P:positive regulation of smooth muscle contra. . .; TAS.  
 KW Bradykinin; Vasodilator.  
 FT PEPTIDE 1 11 MEGASCOLIAKININ.  
 FT PEPTIDE 1 9 BRADYKININ-LIKE PEPTIDE.  
 SQ SEQUENCE 11 AA; 1273 MW; 33867393D771A9C8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RK 8  
 ||  
 Db 9 RK 10

RESULT 3  
 NXSN\_PSETE  
 ID NXSN\_PSETE STANDARD; PRT; 11 AA.  
 AC P59072;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Short neurotoxin N1 (Alpha neurotoxin) (Fragment).  
 OS *Pseudonaja textilis* (Eastern brown snake).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Elapidae; Acanthophiinae; *Pseudonaja*.  
 OX NCBI\_TaxID=8673;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;  
 RX MEDLINE=99449602; PubMed=10518793;  
 RA Gong N.L., Armugam A., Jeyaseelan K.;  
 RT "Postsynaptic short-chain neurotoxins from *Pseudonaja textilis*: cDNA  
 RT cloning, expression and protein characterization.";

RL Eur. J. Biochem. 265:982-989(1999).  
CC -!- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic  
CC acetylcholine receptors (nAChR).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.  
CC -!- MASS SPECTROMETRY: MW=6236; METHOD=Electrospray.  
CC -!- MISCELLANEOUS: LD(50) is 0.84 mg/kg by intravenous injection.  
CC -!- SIMILARITY: Belongs to the snake toxin family.  
DR InterPro; IPR003571; Snake\_toxin.  
DR PROSITE; PS00272; SNAKE\_TOXIN; PARTIAL.  
KW Toxin; Neurotoxin; Postsynaptic neurotoxin;  
KW Acetylcholine receptor inhibitor; Multigene family.  
FT UNSURE 3 3  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1319 MW; 0D1EF0C81B58732B CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10  
||  
Db 9 DT 10

RESULT 4  
PKC1\_CARMO  
ID PKC1\_CARMO STANDARD; PRT; 11 AA.  
AC P82684;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pyrokinin-1 (Cam-PK-1) (FXPRL-Amide).  
OS Carausius morosus (Indian stick insect).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatoidea;  
OC Heteronemiidae; Carausius.  
OX NCBI\_TaxID=7022;  
RN [1]  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RC TISSUE=Corpora cardiaca;  
RA Predel R., Kellner R., Gaede G.;  
RT "Myotropic neuropeptides from the retrocerebral complex of the stick  
insect, Carausius morosus (Phasmatodea: Lonchodidae).";  
RL Eur. J. Entomol. 96:275-278(1999).  
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic  
CC activity).  
CC -!- MASS SPECTROMETRY: MW=1235; METHOD=MALDI.  
CC -!- SIMILARITY: Belongs to the pyrokinin family.  
DR InterPro; IPR001484; Pyrokinin.  
DR PROSITE; PS00539; PYROKININ; FALSE\_NEG.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1236 MW; 2BFA5225BB46C1A8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TQ 11  
||  
Db 5 TQ 6

RESULT 5

PQQC\_PSEFL

ID PQQC\_PSEFL STANDARD; PRT; 11 AA.  
AC P55173;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Coenzyme PQQ synthesis protein C (Pyrroloquinoline quinone biosynthesis protein C) (Fragment).  
GN PQQC.  
OS Pseudomonas fluorescens.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=294;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CHA0;  
RX MEDLINE=96064397; PubMed=8526497;  
RA Schnider U., Keel C., Defago G., Haas D.;  
RT "Tn5-directed cloning of pqq genes from Pseudomonas fluorescens CHA0: mutational inactivation of the genes results in overproduction of the antibiotic pyoluteorin."  
RL Appl. Environ. Microbiol. 61:3856-3864(1995).  
CC --!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.  
CC --!- SIMILARITY: Belongs to the pqqC family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X87299; CAA60734.1; -.  
DR PIR; S58244; S58244.  
DR HAMAP; MF\_00654; -; 1.  
KW PQQ biosynthesis.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1182 MW; 89DF46E4C5B73771 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DT 10  
||  
Db 3 DT 4

## RESULT 6

## Q2OA\_COMTE

ID Q2OA\_COMTE STANDARD; PRT; 11 AA.  
 AC P80464;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Quinoline 2-oxidoreductase, alpha chain (EC 1.3.99.17) (Fragment).  
 OS Comamonas testosteroni (Pseudomonas testosteroni).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Comamonadaceae; Comamonas.  
 OX NCBI\_TaxID=285;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=63;  
 RX MEDLINE=96035889; PubMed=7556204;  
 RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;  
 RT "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from Comamonas testosteroni 63. The first two enzymes in quinoline and 3-methylquinoline degradation.";  
 RL Eur. J. Biochem. 232:536-544(1995).  
 CC -!- FUNCTION: Converts (3-methyl)-quinoline to (3-methyl)-2-oxo-1,2-dihydroquinoline.  
 CC -!- CATALYTIC ACTIVITY: Quinoline + acceptor + H(2)O = isoquinolin-1(2H)-one + reduced acceptor.  
 CC -!- COFACTOR: FAD, molybdenum and iron-sulfur.  
 CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)quinoline; first step.  
 CC -!- SUBUNIT: Heterohexamer of two alpha chains, two beta chains, and two gamma chains (Probable).  
 DR PIR; S66606; S66606.  
 KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1213 MW; 869094322B1DC2CA CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2  
 ||  
 Db 1 AK 2

## RESULT 7

## TKNA\_RANRI

ID TKNA\_RANRI STANDARD; PRT; 11 AA.  
 AC P29207;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ranakinin (Substance-P-related peptide).  
 OS Rana ridibunda (Laughing frog) (Marsh frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8406;  
 RN [1]

RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=92044543; PubMed=1658233;  
RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;  
RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with  
RT neurokinin B from the brain of the frog *Rana ridibunda*.";  
RL J. Neurochem. 57:2086-2091(1991).  
CC -!-- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!-- SUBCELLULAR LOCATION: Secreted.  
CC -!-- SIMILARITY: Belongs to the tachykinin family.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR InterPro; IPR008215; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1352 MW; 3A2460CC59D40B07 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ER 5  
||  
Db 5 ER 6

RESULT 8  
TKND\_RANCA  
ID TKND\_RANCA STANDARD; PRT; 11 AA.  
AC P22691;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ranatachykinin D (RTK D).  
OS *Rana catesbeiana* (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; *Rana*.  
OX NCBI\_TaxID=8400;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Intestine;  
RX MEDLINE=91254337; PubMed=2043143;  
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;  
RT "Isolation of four novel tachykinins from frog (*Rana catesbeiana*)  
RT brain and intestine.";  
RL Biochem. Biophys. Res. Commun. 177:588-595(1991).  
RN [2]  
RP SEQUENCE.  
RC TISSUE=Intestine;  
RX MEDLINE=94023216; PubMed=8210506;  
RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;  
RT "Four novel tachykinins in frog (*Rana catesbeiana*) brain and

RT intestine.";  
RL Regul. Pept. 46:81-88(1993).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; D61033; D61033.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR PROSITE; PS00267; TACHYKININ; FALSE\_NEG.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1350 MW; 3A34256C59D40B07 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ER 5  
||  
Db 5 ER 6

#### RESULT 9

TKN\_ELEMO  
ID TKN\_ELEMO STANDARD; PRT; 11 AA.  
AC P01293;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Eledoisin.  
OS Eledone moschata (Musky octopus) (Ozaena moschata), and  
OS Eledone cirrhosa (Curled octopus) (Ozaena cirrosa).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Eledone.  
OX NCBI\_TaxID=6641, 102876;  
RN [1]  
RP SEQUENCE.  
RA Anastasi A., Erspamer V.;  
RT "The isolation and amino acid sequence of eledoisin, the active  
RT endecapeptide of the posterior salivary glands of Eledone.";  
RL Arch. Biochem. Biophys. 101:56-65(1963).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; A01561; EOCO.  
DR PIR; B01561; EOCC.  
DR PDB; 1MXQ; 18-FEB-03.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation; Pyrrolidone carboxylic acid;  
KW 3D-structure.

FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1206 MW; 570D7C2559CDDAA3 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KD 9  
||  
Db 4 KD 5

RESULT 10

UXB2\_YEAST

ID UXB2\_YEAST STANDARD; PRT; 11 AA.  
AC P99013;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page (Spot 2D-000K2F) (Fragment).  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=X2180-1A;  
RA Sanchez J.-C., Golaz O., Schaller D., Morch F., Frutiger S.,  
RA Hughes G.J., Appel R.D., Deshusses J., Hochstrasser D.F.;  
RL Submitted (AUG-1995) to Swiss-Prot.  
CC --! MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
CC protein is: 6.20, its MW is: 9.2 kDa.  
DR SWISS-2DPAGE; P99013; YEAST.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1328 MW; EC38021C0DCB42DA CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RK 8  
||  
Db 8 RK 9

RESULT 11

ANGT\_CRIGE

ID ANGT\_CRIGE STANDARD; PRT; 11 AA.  
AC P09037;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Crinia-angiotensin II.  
OS Crinia georgiana (Quacking frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;

OC Myobatrachinae; Crinia.  
OX NCBI\_TaxID=8374;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=80024575; PubMed=488254;  
RA Erspamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;  
RT "Amino acid composition and sequence of crinia-angiotensin, an  
RT angiotensin II-like endecapeptide from the skin of the Australian  
RT frog Crinia georgiana.";  
RL Experientia 35:1132-1133(1979).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
DR PIR; S07207; S07207.  
KW Vasoconstrictor.  
SQ SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;

Query Match 9.18; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
|  
Db 1 A 1

RESULT 12  
ASL1\_BACSE  
ID ASL1\_BACSE STANDARD; PRT; 11 AA.  
AC P83146;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Acharan sulfate lyase 1 (EC 4.2.2.-) (Fragment).  
OS Bacteroides stercoris.  
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
OC Bacteroidaceae; Bacteroides.  
OX NCBI\_TaxID=46506;  
RN [1]  
RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.  
RC STRAIN=HJ-15;  
RX MEDLINE=21223019; PubMed=11322884;  
RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;  
RT "Purification and characterization of acharan sulfate lyases, two  
RT novel heparinases, from Bacteroides stercoris HJ-15.";  
RL Eur. J. Biochem. 268:2635-2641(2001).  
CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,  
CC heparin and heparan sulfate.  
CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and cobalt.  
CC Activated by reducing agents, such as DL-dithiothreitol and 2-  
CC mercaptoethanol.  
CC -!- SUBUNIT: Monomer.  
CC -!- PTM: The N-terminus is blocked.  
CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is  
CC 7.2 and optimum temperature 45 degrees Celsius.  
KW Lyase; Heparin-binding.  
FT NON\_TER 1 1

FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1395 MW; 01B2DAA241E865AB CRC64;  
Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6  
|  
Db 11 Q 11

RESULT 13  
BPP3\_BOTIN  
ID BPP3\_BOTIN STANDARD PRT; 11 AA.  
AC P30423;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting  
DE enzyme inhibitor).  
OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8723;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=90351557; PubMed=2386615;  
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
RT "Primary structure and biological activity of bradykinin potentiating  
RT peptides from Bothrops insularis snake venom.";  
RL J. Protein Chem. 9:221-227(1990).  
CC -!- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of  
CC bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; C37196; C37196.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6  
|  
Db 1 Q 1

RESULT 14  
BPP4\_BOTIN  
ID BPP4\_BOTIN STANDARD PRT; 11 AA.  
AC P30424;  
DT 01-APR-1993 (Rel. 25, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting  
DE enzyme inhibitor).  
OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8723;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=90351557; PubMed=2386615;  
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
RT "Primary structure and biological activity of bradykinin potentiating  
RT peptides from Bothrops insularis snake venom.";  
RL J. Protein Chem. 9:221-227(1990).  
CC -!- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of  
CC bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; D37196; D37196.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 11 AA; 1143 MW; 20BBBF13C7741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6  
|  
Db 1 Q 1

RESULT 15  
BPPB\_AGKHA  
ID BPPB\_AGKHA STANDARD; PRT; 11 AA.  
AC P01021;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide B (Angiotensin-converting  
DE enzyme inhibitor).  
OS Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Gloydius.  
OX NCBI\_TaxID=242054;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RA Kato H., Suzuki T.;  
RT "Amino acid sequence of bradykinin-potentiating peptide isolated from  
RT the venom of Agkistrodon halys blomhoffii.";  
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).  
CC -!- FUNCTION: This peptide both inhibits the activity of the

CC        angiotensin-converting enzyme and enhances the action of  
 CC        bradykinin by inhibiting the kinases that inactivate it.  
 CC        It acts as an indirect hypotensive agent.  
 DR        PIR; A01254; XASNBA.  
 KW        Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT        MOD\_RES        1        1        PYRROLIDONE CARBOXYLIC ACID.  
 SQ        SEQUENCE      11 AA;    1199 MW;    295CBF0627741777 CRC64;  
  
 Query Match                9.1%;    Score 1;    DB 1;    Length 11;  
 Best Local Similarity    100.0%;   Pred. No. 9.2e+04;  
 Matches        1;    Conservative    0;    Mismatches    0;    Indels        0;    Gaps        0;  
  
 Qy        6 Q 6  
 |  
 Db        1 Q 1

RESULT 16  
 BPP\_AGKHP  
 ID    BPP\_AGKHP        STANDARD;        PRT;        11 AA.  
 AC    P04562;  
 DT    13-AUG-1987 (Rel. 05, Created)  
 DT    01-FEB-1994 (Rel. 28, Last sequence update)  
 DT    28-FEB-2003 (Rel. 41, Last annotation update)  
 DE    Bradykinin-potentiating peptide (Angiotensin-converting  
 DE    enzyme inhibitor).  
 OS    Agkistrodon halys pallas (Chinese water mocassin) (Gloydius halys  
 OS    pallas).  
 OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC    Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC    Viperidae; Crotalinae; Gloydius.  
 OX    NCBI\_TaxID=8714;  
 RN    [1]  
 RP    SEQUENCE.  
 RC    TISSUE=Venom;  
 RX    MEDLINE=86177022; PubMed=3008123;  
 RA    Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;  
 RT    "Structure-function studies on the bradykinin potentiating peptide  
 RT    from Chinese snake venom (Agkistrodon halys pallas).";  
 RL    Peptides 6 Suppl. 3:339-342(1985).  
 CC    -!- FUNCTION: This peptide both inhibits the activity of the  
 CC    angiotensin-converting enzyme and enhances the action of  
 CC    bradykinin by inhibiting the kinases that inactivate it.  
 CC    It acts as an indirect hypotensive agent.  
 DR    PIR; JC0002; XAVIBH.  
 KW    Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT    MOD\_RES        1        1        PYRROLIDONE CARBOXYLIC ACID.  
 SQ    SEQUENCE      11 AA;    1112 MW;    30BABF1277686777 CRC64;  
  
 Query Match                9.1%;    Score 1;    DB 1;    Length 11;  
 Best Local Similarity    100.0%;   Pred. No. 9.2e+04;  
 Matches        1;    Conservative    0;    Mismatches    0;    Indels        0;    Gaps        0;  
  
 Qy        6 Q 6  
 |  
 Db        1 Q 1

RESULT 17

CA21\_LITCI

ID CA21\_LITCI STANDARD; PRT; 11 AA.

AC P82087;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Caerulein 2.1/2.1Y4.

OS Litoria citropa (Australian blue mountains tree frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;

OC Pelodryadinae; Litoria.

OX NCBI\_TaxID=94770;

RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Skin secretion;

RX MEDLINE=20057701; PubMed=10589099;

RA Wabnitz P.A., Bowie J.H., Tyler M.J.;

RT "Caerulein-like peptides from the skin glands of the Australian blue

RT montains tree frog Litoria citropa. Part 1. Sequence determination

RT using electrospray mass spectrometry.";

RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).

CC -!- FUNCTION: Hypotensive neuropeptide (Probable).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin dorsal glands.

CC -!- PTM: Isoform 2.1Y4 differs from isoform 2.1 in not being

CC sulfated.

CC -!- MASS SPECTROMETRY: MW=1372; METHOD=Electrospray.

CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

DR InterPro; IPR001651; Gastrin.

DR PROSITE; PS00259; GASTRIN; FALSE\_NEG.

KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;

KW Pyrrolidone carboxylic acid.

FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD\_RES 4 4 SULFATION.

FT MOD\_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1312 MW; 10DAB7C4EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.2e+04;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6

Db 1 Q 1

RESULT 18

CA22\_LITCI

ID CA22\_LITCI STANDARD; PRT; 11 AA.

AC P82088;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Caerulein 2.2/2.2Y4.

OS Litoria citropa (Australian blue mountains tree frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
OC Pelodryadinae; Litoria.  
OX NCBI\_TaxID=94770;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RX MEDLINE=20057701; PubMed=10589099;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
RT "Caerulein-like peptides from the skin glands of the Australian blue  
mountains tree frog Litoria citropa. Part 1. Sequence determination  
using electrospray mass spectrometry.";  
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
CC -!- PTM: Isoform 2.2Y4 differs from isoform 2.2 in not being  
sulfated.  
CC -!- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.  
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
DR InterPro; IPR001651; Gastrin.  
DR PROSITE; PS00259; GASTRIN; FALSE\_NEG.  
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 4 4 SULFATION.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1328 MW; 10DAB894EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6  
|  
Db 1 Q 1

RESULT 19  
CA31\_LITCI  
ID CA31\_LITCI STANDARD; PRT; 11 AA.  
AC P82089;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Caerulein 3.1/3.1Y4.  
OS Litoria citropa (Australian blue mountains tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
OC Pelodryadinae; Litoria.  
OX NCBI\_TaxID=94770;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RX MEDLINE=20057701; PubMed=10589099;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
RT "Caerulein-like peptides from the skin glands of the Australian blue

RT montains tree frog *Litoria citropa*. Part 1. Sequence determination  
RT using electrospray mass spectrometry.";  
RL *Rapid Commun. Mass Spectrom.* 13:2498-2502(1999).  
CC -!-- FUNCTION: Hypotensive neuropeptide (Probable).  
CC -!-- SUBCELLULAR LOCATION: Secreted.  
CC -!-- TISSUE SPECIFICITY: Skin dorsal glands.  
CC -!-- PTM: Isoform 3.1Y4 differs from isoform 3.1 in not being  
CC sulfated.  
CC -!-- MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.  
CC -!-- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
DR InterPro; IPR001651; Gastrin.  
DR PROSITE; PS00259; GASTRIN; FALSE\_NEG.  
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 4 4 SULFATION.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1347 MW; 10DAB7D67861A86B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6  
|  
Db 1 Q 1

RESULT 20  
CA32\_LITCI  
ID CA32\_LITCI STANDARD; PRT; 11 AA.  
AC P82090;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Caerulein 3.2/3.2Y4.  
OS *Litoria citropa* (Australian blue mountains tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
OC Pelodryadinae; Litoria.  
OX NCBI\_TaxID=94770;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RX MEDLINE=20057701; PubMed=10589099;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
RT "Caerulein-like peptides from the skin glands of the Australian blue  
RT montains tree frog *Litoria citropa*. Part 1. Sequence determination  
RT using electrospray mass spectrometry.";  
RL *Rapid Commun. Mass Spectrom.* 13:2498-2502(1999).  
CC -!-- FUNCTION: Hypotensive neuropeptide (Probable).  
CC -!-- SUBCELLULAR LOCATION: Secreted.  
CC -!-- TISSUE SPECIFICITY: Skin dorsal glands.  
CC -!-- PTM: Isoform 3.2Y4 differs from isoform 3.2 in not being  
CC sulfated.  
CC -!-- MASS SPECTROMETRY: MW=1423; METHOD=Electrospray.  
CC -!-- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

DR InterPro; IPR001651; Gastrin.  
DR PROSITE; PS00259; GASTRIN; FALSE NEG.  
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 4 4 SULFATION.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1363 MW; 10DAB8867861A86B CRC64;  
  
Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6  
|  
Db 1 Q 1

RESULT 21  
CA41\_LITCI  
ID CA41\_LITCI STANDARD; PRT; 11 AA.  
AC P82091;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Caerulein 4.1/4.1Y4.  
OS Litoria citropa (Australian blue mountains tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
OC Pelodryadinae; Litoria.  
OX NCBI\_TaxID=94770;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RX MEDLINE=20057701; PubMed=10589099;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
RT "Caerulein-like peptides from the skin glands of the Australian blue  
RT montains tree frog Litoria citropa. Part 1. Sequence determination  
RT using electrospray mass spectrometry.";  
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
CC -!-- FUNCTION: Hypotensive neuropeptide (Probable).  
CC -!-- SUBCELLULAR LOCATION: Secreted.  
CC -!-- TISSUE SPECIFICITY: Skin dorsal glands.  
CC -!-- PTM: Isoform 4.1Y4 differs from isoform 4.1 in not being  
CC sulfated.  
CC -!-- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.  
CC -!-- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
DR InterPro; IPR001651; Gastrin.  
DR PROSITE; PS00259; GASTRIN; FALSE NEG.  
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 4 4 SULFATION.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1328 MW; 10DAB7C4F5B861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6  
|  
Db 1 Q 1

RESULT 22

CA42\_LITCI

ID CA42\_LITCI STANDARD; PRT; 11 AA.  
AC P82092;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Caerulein 4.2/4.2Y4.  
OS Litoria citropa (Australian blue mountains tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
OC Pelodryadinae; Litoria.  
OX NCBI\_TaxID=94770;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RX MEDLINE=20057701; PubMed=10589099;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
RT "Caerulein-like peptides from the skin glands of the Australian blue  
RT montains tree frog Litoria citropa. Part 1. Sequence determination  
RT using electrospray mass spectrometry.";  
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
CC --!- FUNCTION: Hypotensive neuropeptide (Probable).  
CC --!- SUBCELLULAR LOCATION: Secreted.  
CC --!- TISSUE SPECIFICITY: Skin dorsal glands.  
CC --!- PTM: Isoform 4.2Y4 differs from isoform 4.2 in not being  
CC sulfated.  
CC --!- MASS SPECTROMETRY: MW=1404; METHOD=Electrospray.  
CC --!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
DR InterPro; IPR001651; Gastrin.  
DR PROSITE; PS00259; GASTRIN; FALSE\_NEG.  
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 4 4 SULFATION.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1344 MW; 10DAB894F5B861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6  
|  
Db 1 Q 1

RESULT 23

CEP1\_ACHFU

ID CEP1\_ACHFU STANDARD; PRT; 11 AA.  
AC P22790;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-DEC-1992 (Rel. 24, Last annotation update)  
DE Cardio-excitatory peptide-1 (ACEP-1).  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=Ferussac; TISSUE=Heart atrium;  
RX MEDLINE=90211261; PubMed=2322251;  
RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;  
RT "A novel cardio-excitatory peptide isolated from the atria of the  
RT African giant snail, *Achatina fulica*."  
RL Biochem. Biophys. Res. Commun. 167:777-783(1990).  
CC -!- FUNCTION: Potentiates the beat of the ventricle, and has also  
CC excitatory actions on the penis retractor muscle, the buccal  
CC muscle and the identified neurons controlling the buccal muscle  
CC movement of achatina.  
CC -!- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.  
DR PIR; A34662; A34662.  
KW Hormone; Amidation.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 Q 6  
|  
Db 3 Q 3

RESULT 24  
CORZ\_PERAM  
ID CORZ\_PERAM STANDARD; PRT; 11 AA.  
AC P11496;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Corazonin.  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=89325572; PubMed=2753132;  
RA Veenstra J.A.;  
RT "Isolation and structure of corazonin, a cardioactive peptide from  
RT the American cockroach.";

RL FEBS Lett. 250:231-234(1989).  
CC -!- FUNCTION: Cardioactive peptide. Corazonin is probably involved  
CC in the physiological regulation of the heart beat.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
DR PIR; S05002; S05002.  
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1387 MW; C7CFF32D6415AB46 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6  
|  
Db 1 Q 1

RESULT 25  
COXA\_CANFA  
ID COXA\_CANFA STANDARD; PRT; 11 AA.  
AC P99501;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).  
GN COX5A.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Heart;  
RX MEDLINE=98163340; PubMed=9504812;  
RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
RT dog heart proteins.";  
RL Electrophoresis 18:2795-2802(1997).  
CC -!- FUNCTION: This is the heme A-containing chain of cytochrome c  
CC oxidase, the terminal oxidase in mitochondrial electron transport.  
CC -!- CATALYTIC ACTIVITY: 4 ferrocyanide c + O<sub>2</sub> = 4 ferricytochrome  
CC c + 2 H<sub>2</sub>O.  
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase Va family.  
DR HSC-2DPAGE; P99501; DOG.  
DR InterPro; IPR003204; Cyt\_c\_ox5A.  
DR Pfam; PF02284; COX5A; 1.  
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1274 MW; 910B35C5B1AB11F5 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 E 4  
|  
Db 6 E 6

RESULT 26  
CSI5\_BACSU  
ID CSI5\_BACSU STANDARD; PRT; 11 AA.  
AC P81095;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cold shock protein CSI5 (11 kDa cold shock protein) (Fragment).  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=168 / JH642;  
RA Graumann P.L., Schmid R., Marahiel M.A.;  
RL Submitted (OCT-1997) to Swiss-Prot.  
RN [2]  
RP CHARACTERIZATION.  
RC STRAIN=168 / JH642;  
RX MEDLINE=96345629; PubMed=8755892;  
RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;  
RT "Cold shock stress-induced proteins in Bacillus subtilis.";  
RL J. Bacteriol. 178:4611-4619(1996).  
CC --!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC --!- INDUCTION: In response to low temperature.  
CC --!- CAUTION: Could not be found in the genome of B.subtilis 168.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1360 MW; 15F6ECEE6322C330 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5  
|  
Db 2 R 2

RESULT 27  
CX5A\_CONAL  
ID CX5A\_CONAL STANDARD; PRT; 11 AA.  
AC P58848;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Conotoxin au5a.  
OS Conus aulicus (Court cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=89437;  
RN [1]

RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
RC TISSUE=Venom;  
RX MEDLINE=99452958; PubMed=10521453;  
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,  
RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,  
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;  
RT "The T-superfamily of conotoxins.";  
RL J. Biol. Chem. 274:30664-30671(1999).  
RN [2]  
RP ERRATUM.  
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,  
RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,  
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;  
RL J. Biol. Chem. 274:36030-36030(1999).  
CC --!- FUNCTION: Causes dorsal fins drooping in fish. No effect is  
CC observed when injected into mice.  
CC --!- SUBCELLULAR LOCATION: Secreted.  
CC --!- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC --!- MASS SPECTROMETRY: MW=1436.6; METHOD=LSIMS.  
CC --!- SIMILARITY: Belongs to the conotoxin T-superfamily.  
DR PIR; A59146; A59146.  
KW Toxin.  
FT DISULFID 2 9  
FT DISULFID 3 10  
SQ SEQUENCE 11 AA; 1441 MW; 21A36775440059D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5  
|  
Db 7 R 7

RESULT 28  
CX5B\_CONAL  
ID CX5B\_CONAL STANDARD; PRT; 11 AA.  
AC P58849;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Conotoxin au5b.  
OS Conus aulicus (Court cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=89437;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Venom;  
RX MEDLINE=99452958; PubMed=10521453;  
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,  
RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,  
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;  
RT "The T-superfamily of conotoxins.";  
RL J. Biol. Chem. 274:30664-30671(1999).

RN [2]  
RP ERRATUM.  
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,  
RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,  
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;  
RL J. Biol. Chem. 274:36030-36030(1999).  
CC -!-- FUNCTION: Causes dorsal fins drooping in fish. No effect is  
CC observed when injected into mice (By similarity).  
CC -!-- SUBCELLULAR LOCATION: Secreted.  
CC -!-- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -!-- MASS SPECTROMETRY: MW=1388.6; METHOD=LSIMS.  
CC -!-- SIMILARITY: Belongs to the conotoxin T-superfamily.  
DR PIR; B59146; B59146.  
KW Toxin.  
FT DISULFID 2 9  
FT DISULFID 3 10  
SQ SEQUENCE 11 AA; 1393 MW; 21A36775440042D7 CRC64;  
  
Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5  
|  
Db 7 R 7

RESULT 29  
CXL1\_CONMR  
ID CXL1\_CONMR STANDARD; PRT; 11 AA.  
AC P58807;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Lambda-conotoxin CMrVIA.  
OS Conus marmoreus (Marble cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=42752;  
RN [1]  
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
RC TISSUE=Venom;  
RX MEDLINE=20564325; PubMed=10988292;  
RA Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,  
RA Seow K.T., Bay B.-H.;  
RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide  
RT pattern and protein folding. Isolation and characterization from the  
RT venom of Conus marmoreus.";  
RL J. Biol. Chem. 275:39516-39522(2000).  
CC -!-- FUNCTION: Inhibits the neuronal noradrenaline transporter.  
CC -!-- SUBCELLULAR LOCATION: Secreted.  
CC -!-- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -!-- MASS SPECTROMETRY: MW=1237.93; MW\_ERR=0.21; METHOD=Electrospray.  
CC -!-- SIMILARITY: Belongs to the chi/lambda-conotoxin family.  
KW Neurotoxin; Toxin; Hydroxylation.  
FT DISULFID 2 11

FT DISULFID 3 8  
FT MOD\_RES 10 10 HYDROXYLATION.  
SQ SEQUENCE 11 AA; 1226 MW; 277AAC60B7232B58 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2  
|  
Db 6 K 6

RESULT 30

EFG\_CLOPA

ID EFG\_CLOPA STANDARD; PRT; 11 AA.  
AC P81350;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Elongation factor G (EF-G) (CP 5) (Fragment).  
GN FUSA.  
OS Clostridium pasteurianum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1501;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=W5;  
RX MEDLINE=98291870; PubMed=9629918;  
RA Flengsrud R., Skjeldal L.;  
RT "Two-dimensional gel electrophoresis separation and N-terminal  
RT sequence analysis of proteins from Clostridium pasteurianum W5.";  
RL Electrophoresis 19:802-806(1998).  
CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of  
CC the nascent protein chain from the A-site to the P-site of the  
CC ribosome.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.  
CC EF-G/EF-2 subfamily.  
DR InterPro; IPR000795; EF\_GTPbind.  
DR PROSITE; PS00301; EFACTOR\_GTP; PARTIAL.  
KW Elongation factor; Protein biosynthesis; GTP-binding.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2  
|  
Db 1 K 1

RESULT 31

ES1\_RAT

ID ES1\_RAT STANDARD; PRT; 11 AA.  
AC P56571;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE ES1 protein, mitochondrial (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=Wistar; TISSUE=Heart;  
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,  
RA Jungblut P.R.;  
RL Submitted (SEP-1998) to Swiss-Prot.  
CC -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).  
CC -!- MISCELLANEOUS: By 2D-PAGE, the determined pI of this protein (spot  
CC P2) is: 8.9, its MW is: 25 kDa.  
CC -!- SIMILARITY: BELONGS TO THE ES1 FAMILY.  
KW Mitochondrion.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1142 MW; D862272D32C72DC2 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5  
|  
Db 1 R 1

RESULT 32  
FAR6\_PENMO  
ID FAR6\_PENMO STANDARD; PRT; 11 AA.  
AC P83321;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRFamide-like neuropeptide FLP6 (DGRTPALRLRF-amide).  
OS Penaeus monodon (Penaeid shrimp).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
OC Penaeidae; Penaeus.  
OX NCBI\_TaxID=6687;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Eyestalk;  
RX MEDLINE=21956277; PubMed=11959015;  
RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,  
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;  
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk  
RT of the giant tiger prawn Penaeus monodon.";  
RL Comp. Biochem. Physiol. 131B:325-337(2002).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- MASS SPECTROMETRY: MW=1301.8; METHOD=MALDI.

CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
CC family.  
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1301 MW; 9A19C860072DC771 CRC64;  
  
Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 9 D 9  
|  
Db 1 D 1

RESULT 33  
FAR9\_CALVO  
ID FAR9\_CALVO STANDARD; PRT; 11 AA.  
AC P41864;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CalliFMRFamide 9.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Thoracic ganglion;  
RX MEDLINE=92196111; PubMed=1549595;  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
RA Rehfeld J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
RT neuropeptides (designated calliFMRFamides) from the blowfly  
RT Calliphora vomitoria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
CC family.  
DR PIR; I41978; I41978.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1359 MW; 8160CE46CAA44321 CRC64;  
  
Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 K 2  
|  
Db 5 K 5

RESULT 34  
HS70\_PINPS

ID HS70\_PINPS STANDARD; PRT; 11 AA.  
 AC P81672;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Heat shock 70 kDa protein (Fragment).  
 OS Pinus pinaster (Maritime pine).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
 OX NCBI\_TaxID=71647;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Needle;  
 RX MEDLINE=99274088; PubMed=10344291;  
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,  
 RA Frigerio J.-M., Plomion C.;  
 RT "Separation and characterization of needle and xylem maritime pine  
 RT proteins.";  
 RL Electrophoresis 20:1098-1108(1999).  
 CC -!-- MISCELLANEOUS: On the 2D-gel the determined pI of this protein  
 CC (spot N164) is: 5.4, its MW is: 73 kDa.  
 CC -!-- SIMILARITY: Belongs to the heat shock protein 70 family.  
 KW ATP-binding; Heat shock; Multigene family.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1228 MW; 037C1BE8DAA44DD0 CRC64;  
  
 Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 4 E 4  
 |  
 Db 2 E 2

RESULT 35  
 LADD\_ONCMY  
 ID LADD\_ONCMY STANDARD; PRT; 11 AA.  
 AC P81018;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Ladderlectin (Fragment).  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Blood;  
 RX MEDLINE=97293418; PubMed=9149391;  
 RA Jensen L.E., Thiel S., Petersen T.E., Jensenius J.C.;  
 RT "A rainbow trout lectin with multimeric structure.";  
 RL Comp. Biochem. Physiol. 116B:385-390(1997).  
 CC -!-- FUNCTION: Lectin that binds sepharose.

CC -!- COFACTOR: Calcium is essential for sepharose binding.  
CC -!- SUBUNIT: Multimeric.  
KW Lectin; Calcium.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1163 MW; 0B26227FF6D45404 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
|  
Db 1 A 1

RESULT 36

LPW\_THETH

ID LPW\_THETH STANDARD; PRT; 11 AA.  
AC P05624;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Trp operon leader peptide.  
GN TRPL.  
OS Thermus thermophilus.  
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;  
OC Thermus.  
OX NCBI\_TaxID=274;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HB8 / ATCC 27634;  
RX MEDLINE=89000781; PubMed=2844259;  
RA Sato S., Nakada Y., Kanaya S., Tanaka T.;  
RT "Molecular cloning and nucleotide sequence of Thermus thermophilus  
RT HB8 trpE and trpG.";  
RL Biochim. Biophys. Acta 950:303-312(1988).  
CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS  
CC OF TRYPTOPHAN.

CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; X07744; CAA30565.1; -.  
KW Tryptophan biosynthesis; Leader peptide.  
SQ SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
|

## RESULT 37

## LSK1\_LEUMA

ID LSK1 LEUMA STANDARD; PRT; 11 AA.  
AC P04428;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Leucosulfakinin-I (LSK-I).  
OS Leucophaea maderae (Madeira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
OC Blaberidae; Leucophaea.  
OX NCBI\_TaxID=6988;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=86315858; PubMed=3749893;  
RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;  
RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to  
RT gastrin and cholecystokinin.";  
RL Science 234:71-73(1986).  
CC --!- FUNCTION: Change the frequency and amplitude of contractions of  
CC the hingut. Inhibits muscle contraction of hindgut.  
CC --!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
DR PIR; A01622; GMROL.  
DR InterPro; IPR001651; Gastrin.  
DR PROSITE; PS00259; GASTRIN; 1.  
KW Hormone; Amidation; Sulfation.  
FT MOD\_RES 6 6 SULFATION.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E86B5AAB CRC64;  
  
Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 4 E 4  
|  
Db 1 E 1

## RESULT 38

## LSKP\_PERAM

ID LSKP\_PERAM STANDARD; PRT; 11 AA.  
AC P36885;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE Perisulfakinin (Pea-SK-I).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978;  
RN [1]

RP SEQUENCE.  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=90137190; PubMed=2615921;  
RA Veenstra J.A.;  
RT "Isolation and structure of two gastrin/CCK-like neuropeptides from  
the American cockroach homologous to the leucosulfakinins.";  
RL *Neuropeptides* 14:145-149(1989).  
CC -!- FUNCTION: Stimulates hindgut contractions.  
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
DR PIR; A60656; A60656.  
DR InterPro; IPR001651; Gastrin.  
DR PROSITE; PS00259; GASTRIN; 1.  
KW Hormone; Amidation; Sulfation.  
FT MOD\_RES 6 6 SULFATION.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAA CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4  
|  
Db 1 E 1

RESULT 39  
MHBI\_KLEPN  
ID MHBI\_KLEPN STANDARD PRT; 11 AA.  
AC P80580;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Maleylpyruvate isomerase (EC 5.2.1.4) (Fragment).  
GN MHBI.  
OS Klebsiella pneumoniae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Klebsiella.  
OX NCBI\_TaxID=573;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96349117; PubMed=8760924;  
RA Robson N.D., Parrott S., Cooper R.A.;  
RT "In vitro formation of a catabolic plasmid carrying Klebsiella  
pneumoniae DNA that allows growth of Escherichia coli K-12 on 3-  
RT hydroxybenzoate.";  
RL *Microbiology* 142:2115-2120(1996).  
CC -!- CATALYTIC ACTIVITY: 3-maleylpyruvate = 3-fumarylpyruvate.  
KW Isomerase.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1387 MW; 1EE0E2DD49C9D5AB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2

Db |  
2 K 2

RESULT 40

MLG\_THETS

ID MLG\_THETS STANDARD; PRT; 11 AA.  
AC P41989;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Melanotropin gamma (Gamma-melanocyte stimulating hormone) (Gamma-MSH).  
OS Theromyzon tessulatum (Leech).  
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
OC Rhynchobellida; Glossiphoniidae; Theromyzon.  
OX NCBI\_TaxID=13286;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=94298944; PubMed=8026574;  
RA Salzet M., Wattez C., Bulet P., Malecha J.;  
RT "Isolation and structural characterization of a novel peptide related  
RT to gamma-melanocyte stimulating hormone from the brain of the leech  
RT Theromyzon tessulatum.";  
RL FEBS Lett. 348:102-106(1994).  
CC -!- SIMILARITY: Belongs to the POMC family.  
DR PIR; S45698; S45698.  
KW Hormone; Amidation.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1486 MW; 2DB8FACE6409C1E8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2

Db 10 K 10

RESULT 41

MORN\_HUMAN

ID MORN\_HUMAN STANDARD; PRT; 11 AA.  
AC P01163;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Morphogenetic neuropeptide (Head activator) (HA).  
OS Homo sapiens (Human),  
OS Rattus norvegicus (Rat),  
OS Bos taurus (Bovine),  
OS Anthopleura elegantissima (Sea anemone), and  
OS Hydra attenuata (Hydra) (Hydra vulgaris).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606, 10116, 9913, 6110, 6087;  
RN [1]

RP SEQUENCE.  
RC SPECIES=Human, Rat, and Bovine;  
RX MEDLINE=82035850; PubMed=7290191;  
RA Bodenmuller H., Schaller H.C.;  
RT "Conserved amino acid sequence of a neuropeptide, the head activator,  
from coelenterates to humans.";  
RL Nature 293:579-580(1981).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=A.elegantissima, and H.attenuata;  
RA Schaller H.C., Bodenmuller H.;  
RT "Isolation and amino acid sequence of a morphogenetic peptide from  
hydra.";  
RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).  
RN [3]  
RP SYNTHESIS.  
RX MEDLINE=82050803; PubMed=7297679;  
RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;  
RT "Synthesis of a new neuropeptide, the head activator from hydra.";  
RL FEBS Lett. 131:317-321(1981).  
RN [4]  
RP FUNCTION.  
RX MEDLINE=90059923; PubMed=2583101;  
RA Schaller H.C., Druffel-Augustin S., Dubel S.;  
RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells  
in the G2/mitosis transition.";  
RL EMBO J. 8:3311-3318(1989).  
CC -!- FUNCTION: HA acts as an autocrine growth factor for neural cells  
CC in the G2/mitosis transition.  
CC -!- CAUTION: This peptide was first isolated from nerve cells of hydra  
CC and was called head activator by the authors, because it induced  
CC head-specific growth and differentiation in this animal. It has  
CC been found in mammalian intestine and hypothalamus.  
DR PIR; A01427; YHRT.  
DR PIR; A93900; YHXAE.  
DR PIR; B01427; YHHU.  
DR PIR; B93900; YHJFHY.  
DR PIR; C01427; YHBO.  
DR GK; P01163; -.  
KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 Q 6  
|  
Db 1 Q 1

RESULT 42  
NUHM\_CANFA  
ID NUHM\_CANFA STANDARD; PRT; 11 AA.  
AC P49820;  
DT 01-OCT-1996 (Rel. 34, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)  
DE (EC 1.6.99.3) (Fragment).  
GN NDUFV2.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Heart;  
RX MEDLINE=98163340; PubMed=9504812;  
RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
RT dog heart proteins.";  
RL Electrophoresis 18:2795-2802(1997).  
CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY  
CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED  
CC TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)  
CC FRAGMENT OF THE ENZYME.  
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.  
CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.  
CC -!- COFACTOR: Binds 1 2Fe-2S cluster (Potential).  
CC -!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.  
CC -!- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the  
CC mitochondrial inner membrane.  
CC -!- SIMILARITY: Belongs to the complex I 24 kDa subunit family.  
DR HSC-2DPAGE; P49820; DOG.  
DR InterPro; IPR002023; Cmplx1\_24kDa.  
DR PROSITE; PS01099; COMPLEX1\_24K; PARTIAL.  
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;  
KW Iron-sulfur; Iron; 2Fe-2S.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1099 MW; 267F5369C9C72DD8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
|  
Db 2 A 2

RESULT 43  
OAIF\_SARBU  
ID OAIF\_SARBU STANDARD; PRT; 11 AA.  
AC P83518;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ovary-derived ACE interactive factor (Neb-ODAIF) [Contains: Neb-  
DE ODAIF(1-9); Neb-ODAIF(1-7)].  
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;

OC Sarcophagidae; Sarcophaga.  
OX NCBI\_TaxID=7385;  
RN [1]  
RP SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND MASS SPECTROMETRY.  
RC TISSUE=Ovary;  
RX MEDLINE=22272747; PubMed=12383874;  
RA Vandingen A., Hens K., Baggerman G., Macours N., Schoofs L.,  
RA De Loof A., Huybrechts R.;  
RT "Isolation and characterization of an angiotensin converting enzyme  
RT substrate from vitellogenic ovaries of *Neobellieria bullata*.";  
RL Peptides 23:1853-1863(2002).  
CC -!- FUNCTION: Substrate for angiotensin converting enzyme (ACE) in  
CC vitro.  
CC -!- PTM: ACE hydrolyzes Neb-ODAIF by sequentially cleaving off two C-  
CC terminal dipeptides.  
CC -!- MASS SPECTROMETRY: MW=1312.7; METHOD=MALDI; RANGE=1-11.  
CC -!- SIMILARITY: To the N-terminal part of insect vitellogenins.  
FT PEPTIDE 1 11 NEB-ODAIF.  
FT PEPTIDE 1 9 NEB-ODAIF(1-9).  
FT PEPTIDE 1 7 NEB-ODAIF(1-7).  
SQ SEQUENCE 11 AA; 1314 MW; 4E114BB566C5A763 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2  
|  
Db 2 K 2

RESULT 44  
PVK1\_PERAM  
ID PVK1\_PERAM STANDARD; PRT; 11 AA.  
AC P41837;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Periviscerokinin-1 (Pea-PVK-1).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Abdominal perisynthetic organs;  
RX MEDLINE=95232021; PubMed=7716075;  
RA Predel R., Linde D., Rapus J., Vettermann S., Penzlin H.;  
RT "Periviscerokinin (Pea-PVK): a novel myotropic neuropeptide from the  
RT perisynthetic organs of the American cockroach.";  
RL Peptides 16:61-66(1995).  
CC -!- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE  
CC HYPERNEURAL MUSCLE.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1114 MW; 39DB5419D7605728 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
|  
Db 2 A 2

RESULT 45

RANC\_RANPI

ID RANC\_RANPI STANDARD; PRT; 11 AA.  
AC P08951;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ranatensin-C.  
OS Rana pipiens (Northern leopard frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
OX NCBI\_TaxID=8404;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=84131098; PubMed=6141890;  
RA Nakajima T.;  
RL Unpublished results, cited by:  
RL Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;  
RL Comp. Biochem. Physiol. 77C:99-108(1984).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin  
CC family.  
DR InterPro; IPR000874; Bombesin.  
DR Pfam; PF02044; Bombesin; 1.  
DR PROSITE; PS00257; BOMBESIN; 1.  
KW Amphibian defense peptide; Bombesin family; Amidation.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1304 MW; D6C9885A61ADC366 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 T 10  
|  
Db 2 T 2

RESULT 46

RE41\_LITRU

ID RE41\_LITRU STANDARD; PRT; 11 AA.  
AC P82074;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Rubellidin 4.1.  
OS *Litoria rubella* (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
OC Pelodryadinae; *Litoria*.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
RA Tyler M.J., Wallace J.C.;  
RT "The structure of new peptides from the Australin red tree frog  
RT '*Litoria rubella*'. The skin peptide profile as a probe for the study  
RT of evolutionary trends of amphibians.";  
RL Aust. J. Chem. 49:955-963(1996).  
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic  
CC activity.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
CC -!- MASS SPECTROMETRY: MW=1039; METHOD=FAB.  
KW Amphibian defense peptide; Amidation.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1040 MW; 84ED5CBC2877205A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 D 9  
|  
Db 4 D 4

RESULT 47  
RR2\_CONAM  
ID RR2\_CONAM STANDARD; PRT; 11 AA.  
AC P42341;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Chloroplast 30S ribosomal protein S2 (Fragment).  
GN RPS2.  
OS *Conopholis americana* (Squawroot).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;  
OC lamiids; Lamiales; Orobanchaceae; Orobancheae; *Conopholis*.  
OX NCBI\_TaxID=4179;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92145776; PubMed=1723664;  
RA Taylor G., Wolfe K.H., Morden C.W., Depamphilis C.W., Palmer J.D.;  
RT "Lack of a functional plastid tRNA(Cys) gene is associated with loss  
RT of photosynthesis in a lineage of parasitic plants.";  
RL Curr. Genet. 20:515-518(1991).  
CC -!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.  
CC -----

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DR EMBL; X64567; CAA45868.1; -.

DR PIR; S32575; S32575.

DR HAMAP; MF\_00291; -; 1.

DR InterPro; IPR001865; Ribosomal\_S2.

DR PROSITE; PS00962; RIBOSOMAL\_S2\_1; PARTIAL.

DR PROSITE; PS00963; RIBOSOMAL\_S2\_2; PARTIAL.

KW Ribosomal protein; Chloroplast.

FT NON\_TER 11 11

SQ SEQUENCE 11 AA; 1497 MW; 76CD719954536B44 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4  
|  
Db 11 E 11

RESULT 48

RRPL\_CHAV

ID RRPL\_CHAV STANDARD; PRT; 11 AA.

AC P13179;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)  
(L protein) (Fragment).

GN L.

OS Chandipura virus (strain I653514).

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

OC Rhabdoviridae; Vesiculovirus.

OX NCBI\_TaxID=11273;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89299473; PubMed=2741347;

RA Masters P.S., Bhella R.S., Butcher M., Patel B., Ghosh H.P.,

RA Banerjee A.K.;

RT "Structure and expression of the glycoprotein gene of Chandipura  
virus.";

RL Virology 171:285-290(1989).

CC -!- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE  
CC POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS  
CC METHYLATION OF CAPS, AND POLY(A) SYNTHESIS.

CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +  
CC {RNA}(N).

CC -!- SUBUNIT: THOUGHT TO FORM A TRANSCRIPTION COMPLEX WITH THE  
CC NUCLEOCAPSID (N) PROTEIN.

CC -!- SIMILARITY: WITH THE L PROTEIN OF OTHER RABDOVIRUSES AND

CC PARAMYXOVIRUSES.

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CC -----

DR EMBL; J04350; AAA42917.1; -.

KW Transferase; RNA-directed RNA polymerase.

FT NON\_TER 11 11

SQ SEQUENCE 11 AA; 1189 MW; 0335D6E3AAB2D764 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 D 9  
|  
Db 2 D 2

RESULT 49

RS30\_ONCMY

ID RS30\_ONCMY STANDARD; PRT; 11 AA.

AC P83328;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE 40S ribosomal protein S30 (Fragment).

GN FAU.

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI\_TaxID=8022;

RN [1]

RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.

RC TISSUE=Skin mucus;

RX MEDLINE=22142142; PubMed=12147245;

RA Fernandes J.M.O., Smith V.J.;

RT "A novel antimicrobial function for a ribosomal peptide from rainbow trout skin.";

RL Biochem. Biophys. Res. Commun. 296:167-171(2002).

CC --!- FUNCTION: Has antibacterial activity against Gram-positive bacteria.

CC --!- MASS SPECTROMETRY: MW=6676.6; METHOD=MALDI.

CC --!- SIMILARITY: Belongs to the S30E family of ribosomal proteins.

KW Ribosomal protein; Antibiotic.

FT NON\_TER 11 11

SQ SEQUENCE 11 AA; 1123 MW; 2312AB630DD735B8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2  
|  
Db 1 K 1

RESULT 50

T2P1\_PROVU

ID T2P1\_PROVU STANDARD; PRT; 11 AA.  
AC P31031;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Type II restriction enzyme Pvul (EC 3.1.21.4) (Endonuclease Pvul)  
DE (R.Pvul) (Fragment).  
GN PVUIR.  
OS Proteus vulgaris.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Proteus.  
OX NCBI\_TaxID=585;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 13315;  
RX MEDLINE=93087186; PubMed=1454536;  
RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;  
RT "Cloning and characterization of genes for the Pvul restriction and  
RT modification system.";  
RL Nucleic Acids Res. 20:5743-5747(1992).  
CC -!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND  
CC CLEAVES AFTER T-4.  
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give  
CC specific double-stranded fragments with terminal 5'-phosphates.  
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CC -----  
DR EMBL; L04163; AAA25660.1; -.  
DR PIR; S35490; S35490.  
DR REBASE; 1541; Pvul.  
KW Restriction system; Hydrolase; Nuclease; Endonuclease.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 D 9  
|  
Db 4 D 4

RESULT 51

TIN1\_HOPTI

ID TIN1\_HOPTI STANDARD; PRT; 11 AA.  
AC P82651;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Tigerinin-1.  
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;  
OC Hoplobatrachus.  
OX NCBI\_TaxID=103373;  
RN [1]  
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.  
RC TISSUE=Skin secretion;  
RX PubMed=11031261;  
RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,  
RA Devi A.S., Nagaraj R., Sitaram N.;  
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana  
RT tigerina.";  
RL J. Biol. Chem. 276:2701-2707(2001).  
CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,  
CC S.aureus, M.luteus, P.putida and S.cerevisiae.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- MASS SPECTROMETRY: MW=1342; METHOD=MALDI.  
KW Amphibian defense peptide; Antibiotic; Fungicide; Amidation.  
FT DISULFID 2 10  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1344 MW; A2087DC960476056 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5  
|  
Db 9 R 9

RESULT 52

TIN4\_HOPTI

ID TIN4\_HOPTI STANDARD; PRT; 11 AA.  
AC P82654;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tigerinin-4.  
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;  
OC Hoplobatrachus.  
OX NCBI\_TaxID=103373;  
RN [1]  
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.  
RC TISSUE=Skin secretion;

RX PubMed=11031261;  
 RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,  
 RA Devi A.S., Nagaraj R., Sitaram N.;  
 RT "Tigerinins: novel antimicrobial peptides from the Indian frog *Rana*  
 RT *tigerina*.";  
 RL *J. Biol. Chem.* 276:2701-2707(2001).  
 CC -!- FUNCTION: Antibacterial activity against *B.subtilis*, *E.coli*,  
 CC *S.aureus*, *M.luteus*, *P.putida* and *S.cerevisiae*.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.  
 KW Amphibian defense peptide; Antibiotic.  
 FT DISULFID 3 11  
 SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5  
 |  
 Db 1 R 1

RESULT 53  
 TKC2\_CALVO  
 ID TKC2\_CALVO STANDARD; PRT; 11 AA.  
 AC P41518;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Callitachykinin II.  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora.  
 OX NCBI\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RX MEDLINE=95075727; PubMed=7984492;  
 RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,  
 RA Naessel D.R.;  
 RT "Callitachykinin I and II, two novel myotropic peptides isolated from  
 RT the blowfly, *Calliphora vomitoria*, that have resemblances to  
 RT tachykinins.";  
 RL Peptides 15:761-768(1994).  
 CC -!- FUNCTION: Myoactive peptide.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1103 MW; 15D7E3F9C9CDD444 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
|  
Db 6 A 6

RESULT 54  
TKN1\_PSEGU  
ID TKN1\_PSEGU STANDARD; PRT; 11 AA.  
AC P42986;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Kassinin-like peptide K-I (PG-KI).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
OC Myobatrachinae; Pseudophryne.  
OX NCBI\_TaxID=30349;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=90287814; PubMed=2356157;  
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
RA Roberts J.D., Melchiorri P., Erspamer V.;  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
RT the Australian frog Pseudophryne guntheri.";  
RL Peptides 11:299-304(1990).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; B60409; B60409.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR InterPro; IPR008215; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6  
|  
Db 1 Q 1

RESULT 55  
TKN1\_UPEIN

ID TKN1\_UPEIN STANDARD; PRT; 11 AA.  
AC P82026;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Uperin 1.1.  
OS Uperoleia inundata (Floodplain toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
OC Myobatrachinae; Uperoleia.  
OX NCBI\_TaxID=104953;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,  
RA Adams G.W., Severini C.;  
RT "Novel uperin peptides from the dorsal glands of the australian  
RT floodplain toadlet Uperoleia inundata.";  
RL Aust. J. Chem. 49:475-484(1996).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
CC -!- MASS SPECTROMETRY: MW=1208; METHOD=FAB.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1226 MW; 3293693E59CDD457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 Q 6  
|  
Db 1 Q 1

RESULT 56  
TKN1\_UPERU  
ID TKN1\_UPERU STANDARD; PRT; 11 AA.  
AC P08612;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Uperolein.  
OS Uperoleia rugosa (Wrinkled toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
OC Myobatrachinae; Uperoleia.

OX NCBI\_TaxID=8368;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=75131227; PubMed=1120493;  
 RA Anastasi A., Erspamer V., Endean R.;  
 RT "Structure of uperolein, a physalaemin-like endecapeptide occurring  
 in the skin of *Uperoleia rugosa* and *Uperoleia marmorata*.";  
 RL *Experientia* 31:394-395(1975).  
 CC -!-- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!-- SUBCELLULAR LOCATION: Secreted.  
 CC -!-- TISSUE SPECIFICITY: Skin.  
 CC -!-- SIMILARITY: Belongs to the tachykinin family.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	6 Q 6
Db	1 Q 1

RESULT 57  
 TKN2\_PSEGU  
 ID TKN2\_PSEGU STANDARD; PRT; 11 AA.  
 AC P42987;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Kassinin-like peptide K-II (PG-KII).  
 OS Pseudophryne guentheri (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachinae; Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RT the Australian frog *Pseudophryne guntheri*.";

RL Peptides 11:299-304 (1990).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; C60409; C60409.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CB1AB7 CRC64;  
  
 Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 6 Q 6  
 |  
 Db 1 Q 1

RESULT 58  
 TKN2\_UPERU  
 ID TKN2\_UPERU STANDARD; PRT; 11 AA.  
 AC P08616;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Rugosauperolein II ([Lys5,Thr6]physalaemin).  
 OS Uperoleia rugosa (Wrinkled toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachinae; Uperoleia.  
 OX NCBI\_TaxID=8368;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=80223080; PubMed=7389029;  
 RA Nakajima T., Yasuhara T., Erspamer V., Erspamer G.F., Negri L.;  
 RT "Physalaemin- and bombesin-like peptides in the skin of the  
 RT Australian leptodactylid frog Uperoleia rugosa.";  
 RL Chem. Pharm. Bull. 28:689-695(1980).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.

DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1270 MW; 3293693E59D1A327 CRC64;  
  
 Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6  
 |  
 Db 1 Q 1

RESULT 59  
 TKN3\_PSEGU  
 ID TKN3\_PSEGU STANDARD; PRT; 11 AA.  
 AC P42988;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Kassinin-like peptide K-III (PG-KIII).  
 OS Pseudophryne guentheri (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachinae; Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RT the Australian frog Pseudophryne guntheri.";  
 RL Peptides 11:299-304(1990).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; D60409; D60409.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1268 MW; 3DBA7C37C9CB1457 CRC64;  
Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6  
|  
Db 1 Q 1

RESULT 60  
TKN4\_PSEGU  
ID TKN4\_PSEGU STANDARD; PRT; 11 AA.  
AC P42989;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Substance P-like peptide I (PG-SPI).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
OC Myobatrachinae; Pseudophryne.  
OX NCBI\_TaxID=30349;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=90287814; PubMed=2356157;  
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
RA Roberts J.D., Melchiorri P., Erspamer V.;  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
RT the Australian frog Pseudophryne guntheri.";  
RL Peptides 11:299-304 (1990).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; E60409; E60409.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR InterPro; IPR008215; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6

Db 1 Q 1

RESULT 61  
TKN5\_PSEGU  
ID TKN5\_PSEGU STANDARD; PRT; 11 AA.  
AC P42990;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Substance P-like peptide II (PG-SPII).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
OC Myobatrachinae; Pseudophryne.  
OX NCBI\_TaxID=30349;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=90287814; PubMed=2356157;  
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
RA Roberts J.D., Melchiorri P., Erspamer V.,  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
RT the Australian frog Pseudophryne guntheri.";  
RL Peptides 11:299-304(1990).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; F60409; F60409.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR InterPro; IPR008215; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;  
  
Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6  
|  
Db 1 Q 1

RESULT 62  
TKNA\_CHICK  
ID TKNA\_CHICK STANDARD; PRT; 11 AA.

AC P19850;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Substance P.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Intestine;  
RX MEDLINE=88204263; PubMed=2452461;  
RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;  
RT "[Arg3]substance P and neurokinin A from chicken small intestine.";  
RL Regul. Pept. 20:171-180(1988).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; JN0023; JN0023.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 R 5  
|  
Db 1 R 1

RESULT 63  
TKNA\_GADMO  
ID TKNA\_GADMO STANDARD; PRT; 11 AA.  
AC P28498;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Substance P.  
OS Gadus morhua (Atlantic cod).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.  
OX NCBI\_TaxID=8049;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=92298992; PubMed=1376687;

RA Jensen J., Conlon J.M.;  
 RT "Substance-P-related and neurokinin-A-related peptides from the brain  
 RT of the cod and trout.";  
 RL Eur. J. Biochem. 206:659-664(1992).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; S23306; S23306.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
 FT MOD\_RES 11 11 AMIDATION (BY SIMILARITY).  
 SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;  
  
 Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 2 K 2  
 |  
 Db 1 K 1

RESULT 64  
 TKNA\_HORSE  
 ID TKNA\_HORSE STANDARD; PRT; 11 AA.  
 AC P01290;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Substance P.  
 GN TAC1 OR NKNA OR TAC2 OR NKA.  
 OS Equus caballus (Horse), and  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796, 10141;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=Horse;  
 RA Studer R.O., Trzeciak A., Lergier W.;  
 RT "Isolation and amino-acid sequence of substance P from horse  
 RT intestine.";  
 RL Helv. Chim. Acta 56:860-866(1973).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=C.porcellus;  
 RX MEDLINE=90044685; PubMed=2478925;  
 RA Murphy R.;  
 RT "Primary amino acid sequence of guinea-pig substance P.";  
 RL Neuropeptides 14:105-110(1989).

CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; A01558; SPHO.  
 DR PIR; A60654; A60654.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C6C7 CRC64;  
  
 Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 5 R 5  
 |  
 Db 1 R 1

RESULT 65  
 TKNA\_ONCMY  
 ID TKNA\_ONCMY STANDARD; PRT; 11 AA.  
 AC P28499;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Substance P.  
 OS *Oncorhynchus mykiss* (Rainbow trout) (*Salmo gairdneri*).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; *Oncorhynchus*.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=92298992; PubMed=1376687;  
 RA Jensen J., Conlon J.M.;  
 RT "Substance-P-related and neurokinin-A-related peptides from the brain  
 RT of the cod and trout.";  
 RL Eur. J. Biochem. 206:659-664(1992).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; S23308; S23308.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.

DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
 FT MOD\_RES 11 11 AMIDATION (BY SIMILARITY).  
 SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;  
  
 Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 2 K 2  
 |  
 Db 1 K 1

RESULT 66  
 TKNA\_RANCA  
 ID TKNA\_RANCA STANDARD; PRT; 11 AA.  
 AC P22688;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ranatachykinin A (RTK A).  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Brain, and Intestine;  
 RX MEDLINE=91254337; PubMed=2043143;  
 RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;  
 RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)  
 RT brain and intestine.";  
 RL Biochem. Biophys. Res. Commun. 177:588-595(1991).  
 RN [2]  
 RP SEQUENCE.  
 RC TISSUE=Intestine;  
 RX MEDLINE=94023216; PubMed=8210506;  
 RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;  
 RT "Four novel tachykinins in frog (Rana catesbeiana) brain and  
 RT intestine.";  
 RL Regul. Pept. 46:81-88(1993).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; A61033; A61033.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1311 MW; 200D60CC59D40AB7 CRC64;  
Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2  
|  
Db 1 K 1

RESULT 67

TKNA\_SCYCA

ID TKNA\_SCYCA STANDARD; PRT; 11 AA.  
AC P41333;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Substance P.  
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;  
OC Scyliorhinidae; Scyliorhinus.  
OX NCBI\_TaxID=7830;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=93292508; PubMed=7685693;  
RA Waugh D., Wang Y., Hazon N., Balment R.J., Conlon J.M.;  
RT "Primary structures and biological activities of substance-P-related  
peptides from the brain of the dogfish, Scyliorhinus canicula.";  
RL Eur. J. Biochem. 214:469-474(1993).  
CC -!-- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!-- SUBCELLULAR LOCATION: Secreted.  
CC -!-- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; S33300; S33300.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1278 MW; 214860DEC9D6D867 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2  
|  
Db 1 K 1

RESULT 68

TKN\_PHYFU

ID TKN\_PHYFU STANDARD; PRT; 11 AA.

AC P08615;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Physalaemin.  
OS Physalaemus fuscumaculatus (Neotropical frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;  
OC Leptodactylinae; Physalaemus.  
OX NCBI\_TaxID=8378;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=66076612; PubMed=5857249;  
RA Erspamer V., Anastasi A., Bertaccini G., Cei J.M.;  
RT "Structure and pharmacological actions of physalaemin, the main  
RT active polypeptide of the skin of Physalaemus fuscumaculatus.";  
RL Experientia 20:489-490(1964).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; S07201; S07201.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1283 MW; 3293693E59C33457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6  
|  
Db 1 Q 1

RESULT 69  
UF05\_MOUSE  
ID UF05\_MOUSE STANDARD; PRT; 11 AA.  
AC P38643;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page of fibroblasts (P48) (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]

RP SEQUENCE.  
RC TISSUE=Fibroblast;  
RX MEDLINE=95009907; PubMed=7523108;  
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
RT "Separation and sequencing of familiar and novel murine proteins  
RT using preparative two-dimensional gel electrophoresis.";  
RL Electrophoresis 15:735-745(1994).  
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
CC protein is: 5.5, its MW is: 48 kDa.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1328 MW; E54835E5CAAABAFA CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2  
|  
Db 1 K 1

RESULT 70  
ULAG\_HUMAN  
ID ULAG\_HUMAN STANDARD; PRT; 11 AA.  
AC P31933;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page of liver tissue (Spot 118) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Liver;  
RX MEDLINE=94147969; PubMed=8313870;  
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,  
RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;  
RT "Human liver protein map: update 1993.";  
RL Electrophoresis 14:1216-1222(1993).  
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
CC protein is: 5.5, its MW is: 34 kDa.  
DR SWISS-2DPAGE; P31933; HUMAN.  
DR Siena-2DPAGE; P31933; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1219 MW; EDABD37F272DDB0A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6  
|  
Db 3 Q 3

Search completed: April 8, 2004, 15:47:19  
Job time : 6.15385 secs